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Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: GARY COUNTS Examiner #: 78696 Date: 7/15/03
 Art Unit: 1641 Phone Number 30 5-1444 Serial Number: 09/923716
 Mail Box and Bldg/Room Location: CM1 7D10 Results Format Preferred (circle): PAPER DISK E-MAIL
 Mail Box: 7E12

If more than one search is submitted, please prioritize searches in order of need:

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.
 Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract:

Title of Invention: Process for detecting serine/threonine Kinase Activity

Inventors (please provide full names): Joaquin Krane, Thomas Mander, Richard Bethel,
Nail Benson

Earliest Priority Filing Date: 8/11/2000

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search

Claim 10 - Seq ID NO: 4

Claim 15 Seq ID NO: 2

Claim 16 Seq ID NO: 1

11

11

11

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Type of Search

Vendors and cost where applicable

Searcher: Hanley NA Sequence (#) B STN _____
 Searcher Phone #: _____ AA Sequence (#) 3 Dialog _____
 Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: 7/16 Bibliographic _____ Dr. Link _____
 Date Completed: 7/17 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: 5 Fulltext _____ Sequence Systems 02
 Clerical Prep Time: 4 Patent Family _____ WWW/Internet _____
 Online Time: 10 Other _____ Other (specify) _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 44.3333 Seconds
(without alignments)
33.062 Million cell updates/sec

Title: US-09-923-716c-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	38	65.5	207	21	Arabidopsis thalia
2	38	65.5	262	18	Plant steroid 5-al
3	38	65.5	262	21	Arabidopsis thalia
4	38	65.5	394	23	Lactococcus lactis
5	37	63.8	560	22	Novel human diagno
6	36	62.1	82	22	Human polypeptide
7	35	60.3	242	21	Arabidopsis thalia
8	35	60.3	244	21	Arabidopsis thalia
9	35	60.3	244	21	Arabidopsis thalia
10	35	60.3	246	21	Soybean neutral tr

11	35	60.3	251	21	AAG07360	Arabidopsis thalia
12	35	60.3	251	21	AAG61262	Arabidopsis thalia
13	35	60.3	252	21	AAG09306	Arabidopsis thalia
14	35	60.3	254	21	AAG09305	Arabidopsis thalia
15	35	60.3	254	22	AAG86353	A. thaliana allene
16	35	60.3	254	23	ABR90980	Herbicidally activ
17	35	60.3	258	21	AAG07359	Arabidopsis thalia
18	35	60.3	258	21	AAG61261	Arabidopsis thalia
19	34	58.6	56	21	AAG55171	Arabidopsis thalia
20	34	58.6	56	21	AAG60760	Arabidopsis thalia
21	34	58.6	57	21	AAG55170	Arabidopsis thalia
22	34	58.6	57	21	AAG60759	Arabidopsis thalia
23	34	58.6	264	21	AAG05880	Arabidopsis thalia
24	34	58.6	264	21	AAG51213	Arabidopsis thalia
25	34	58.6	264	22	AAG78329	Human protein SEQ
26	34	58.6	266	21	AAG51212	Arabidopsis thalia
27	34	58.6	267	21	AAG05879	Arabidopsis thalia
28	34	58.6	322	20	AAV30161	Human dorsal root
29	34	58.6	322	20	AAV30162	Human dorsal root
30	34	58.6	322	22	AAE12794	Human G-protein co
31	34	58.6	322	22	AAU04371	Human G-protein co
32	34	58.6	322	22	AAG64294	Human GTP-binding
33	34	58.6	322	23	AAE21288	Human MrgX1 (mas-I
34	34	58.6	322	23	AAE17074	Human G-protein co
35	34	58.6	591	21	AAV58905	Rhinocladiaella atr
36	34	58.6	598	21	AAV58903	Rhinocladiaella atr
37	33.5	57.8	1810	22	ABB71194	Drosophila melanog
38	33	56.9	99	23	ABP41643	Human ovarian anti
39	33	56.9	310	21	AAE21021	Human nucleic acid
40	33	56.9	593	22	AAU51414	Propionibacterium
41	33	56.9	609	20	AAW82726	Adenovirus PACTSS1
42	33	56.9	609	20	AAW82727	Adenovirus P194KN
43	33	56.9	656	22	AAG50823	C glutamicum prote
44	33	56.9	700	22	AAE28610	Yeast Rf1. Uniden
45	33	56.9	725	22	ABE68684	Drosophila melanog
46	33	56.9	750	20	AAW62728	Adenovirus PNP194
47	33	56.9	1235	23	ABW48680	Listeria monocytog
48	32	55.2	66	22	AAU55532	Propionibacterium
49	32	55.2	72	23	ABP33743	Human ORF2716 prot
50	32	55.2	74	23	AAO21674	Human secreted pro
51	32	55.2	93	22	AAW83247	Human immune/haema
52	32	55.2	137	22	AAU45923	Propionibacterium
53	32	55.2	156	22	AAU65539	Propionibacterium
54	32	55.2	283	23	ABW49253	Listeria monocytog
55	32	55.2	358	23	AAW52346	Hydratase-aldehyde
56	32	55.2	446	20	AAV42113	Corn anthranilate
57	32	55.2	447	22	AAU03135	Streptococcus pyog
58	32	55.2	447	22	AAU03140	Streptococcus pyog
59	32	55.2	447	23	ABP30002	Streptococcus poly
60	32	55.2	462	21	AAV58906	Amino polyol amine
61	32	55.2	462	21	AAV58907	Amino polyol amine
62	32	55.2	462	21	AAV68843	Amino acid sequenc
63	32	55.2	462	21	AAV68844	Amino acid sequenc
64	32	55.2	463	21	AAV58909	Amino polyol amine
65	32	55.2	463	21	AAV68845	Amino acid sequenc
66	32	55.2	487	21	AAV58912	Amino polyol amine
67	32	55.2	487	21	AAV68848	An aminopolylol ami
68	32	55.2	491	20	AAV41302	Tobacco anthranila
69	32	55.2	519	23	ABP27100	Streptococcus poly
70	32	55.2	526	23	ABW26884	Herbicidally activ
71	32	55.2	554	21	AAV58910	Amino polyol amine
72	32	55.2	554	21	AAV68846	An aminopolylol ami
73	32	55.2	577	20	AAW93815	Rice ASA first iso
74	32	55.2	577	20	AAW93810	Rice anthranilate
75	32	55.2	595	23	ABW93363	Herbicidally activ

ALIGNMENTS

RESULT 1
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ID AAG29277 standard; Protein; 207 AA.

XX AAG29277; 18-JUN-1999; 99US-0139462.
AC 18-JUN-1999; 99US-0139463.
XX 18-JUN-1999; 99US-0139750.
DT 18-JUN-1999; 99US-0139763.
XX 21-JUN-1999; 99US-0139817.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34806. 99US-0139899.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence. 99US-0140695.
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 Db 38 RTIIYPLRLFR 48

RESULT 2
 AAW27262
 ID AAW27262 standard; Protein; 262 AA.

XX AC AAW27262;
 XX AC AAW27262;
 DT 23-APR-1998 (first entry)

XX XX Plant steroid 5-alpha reductase DET2.
 XX XX

KW Plant steroid 5-alpha reductase; Arabidopsis; DET2; pest resistance;
 KW brassinolide biosynthesis; growth.
 XX Arabidopsis sp.
 OS Arabidopsis sp.
 PN W09739112-A1.
 XX 23-OCT-1997.
 XX 14-APR-1997; 97WO-US061115.
 XX 18-APR-1996; 96US-0634475.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Chory J, Li J;
 XX WPI; 1997-526449/48.
 DR N-PSDB; AAT91260.
 XX New isolated plant steroid 5-alpha reductase gene, DET2 - used to
 PT develop products for e.g. increasing plant yield and pest resistance
 PT or for producing plants with reduced stature
 XX Claim 4; Page 45-46; 70pp; English.
 XX The present sequence represents a novel plant steroid 5-alpha reductase,
 CC DET2. Methods have also been developed for producing plants with
 CC increased yield, as compared to wild-type. The DET2 polypeptides have
 CC 5AR activity and are involved in the brassinolide biosynthesis pathway.
 CC The products and methods can be used to produce modified plants which
 CC can exhibit increased plant growth, increased crop yield or increased
 CC biomass. The plants can also have increased resistance to pests and
 CC pesticides. Inhibitors of DET2 can be used to cause loss of function of
 CC DET2 resulting in, e.g. male sterile plants or reduced stature (dwarf
 CC plants).
 XX SQ Sequence 262 AA;
 Query Match 65.5%; Score 38; DB 18; Length 262;
 Best Local Similarity 45.5%; Pred. No. 12;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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 Db 93 RTIIYPLRLFR 103
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 ID AAG29276 standard; Protein; 262 AA.
 XX AC AAG29276;
 XX 17-OCT-2000 (first entry)
 DT Arabidopsis thaliana protein fragment SEQ ID NO: 34805.
 DE Arabidopsis thaliana.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN EPI033405-A2.
 XX 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-0301439.
 PF 25-FEB-1999; 99US-0121825.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.

PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
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 PR 14-OCT-1999; 99US-0159637.
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 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
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 PR 25-OCT-1999; 99US-0161404.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.5%; Score 38; DB 21; Length 262;

Best Local Similarity 45.5%; Pred. No. 12;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 RTVYPTMMFK 11
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 Db 93 RTIYPLRLFR 103

RESULT 4
 ABB53569
 ID ABB53569 standard; Protein; 394 AA.

XX ABB53569;

XX 16-MAY-2002 (first entry)

XX Lactococcus lactis protein ycgB.

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

XX Lactococcus lactis IL1403.

XX FR2807446-A1.

XX -12-OCT-2001.

XX 11-APR-2000; 2000FR-0004630.

XX 11-APR-2000; 2000FR-0004630.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX WPI; 2002-043418/06.

XX New nucleotide sequence useful in the identification of Lactococcus
 PT lactis and related species -

XX Claim 6; SEQ ID No 271; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
 CC nucleic acid sequence is useful in the detection and/or amplification of
 CC nucleic acid sequence, particularly to identify Lactococcus lactis or
 CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO200177334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 394 AA;

Query Match 65.5%; Score 38; DB 23; Length 394;

Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 TVVYPTMMF 10
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 Db 47 TLIYPTMRF 55

RESULT 5
 ABG29423
 ID ABG29423 standard; Protein; 560 AA.

XX AC ABG29423;

XX DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #29414.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS93610.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID No 59782; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 560 AA;

Query Match 63.8%; Score 37; DB 22; Length 560;
 Best Local Similarity 77.8%; Pred. NO. 46;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVPTMMF 10

DB 214 TLVPTMMF 222

RESULT 6

ID AAO10186 standard; Protein; 82 AA.

XX AAO10186;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 24078.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

PD 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI90117.

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

PS Claim 20; SEQ ID NO 24078; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 82 AA;

Query Match 62.1%; Score 36; DB 22; Length 82;
 Best Local Similarity 85.7%; Pred. NO. 8.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPTMMFK 11

DB 1 YPTMMFK 7

RESULT 7

ID AAG09307 standard; Protein; 242 AA.

XX AAG09307;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 7187.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126284.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

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PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

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PR 28-JUL-1999; 99US-0145951.
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PR 04-AUG-1999; 99US-0147204.
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PR 06-AUG-1999; 99US-0147303.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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ID	AAG07361 standard; Protein; 244 AA.								
AC	ARG07361;								
XX									
DT	17-OCT-2000 (first entry)								
XX									
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 4485.								
XX									
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.								
KW									
XX									
OS	Arabidopsis thaliana.								
XX									
PN	EPI033405-A2.								
XX									
PD	06-SEP-2000.								
XX									
PF	25-FEB-2000;.2000EP-0301439.								
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Query Match 60.3%; Score 35; DB 21; Length 244;
Best Local Similarity 60.0%; Pred No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
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Db 188 RQLVPTKLF 197

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AC AAAY32315;
XX
DT 28-FEB-2000 (first entry)

XX Soybean neutral triacylglycerol lipase.
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 KW vegetable oil; transgenic plant.
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 XX Glycine max.
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 XX WO9955883-A2.
 PN
 XX
 PD 04-NOV-1999.
 XX
 XX 29-APR-1999; 99WO-US09280.
 PF
 XX 30-APR-1998; 98US-0083688.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Cahoon EB, Cahoon RE, Kinney AJ, Rafalski JA;
 PI WPI; 2000-062036/05.
 XX N-PSDB; AAZ34964.
 DR
 XX Novel plant triacylglycerol lipase polynucleotides used to alter the
 PT level of the enzyme in transgenic plants -
 PT
 XX Claim 10; Page 58-59; 65pp; English.
 PS
 XX This sequence represents most of a soybean neutral triacylglycerol
 CC lipase (TAGL), as deduced from the nucleotide sequence of isolated
 CC cDNA clones (see AAZ34964). Novel acid and neutral TAGL polypeptides
 CC (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,
 CC Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes
 CC may be prepared recombinantly and used to raise antibodies, which
 CC are used for detecting the enzymes in situ in cells or in vitro in
 CC cell extracts. The polynucleotides may be used to create transgenic
 CC plants in which the TAGL levels are present at higher or lower levels
 CC than normal, or in cell types or developmental processes where they are
 CC not normally found. This would alter the level of triacylglycerol and
 CC cholesterol esters found in those cells. Accumulation of fatty acids
 CC with unusual structures may be a positive phenotype in plants used for
 CC foods. In addition, it may be desirable to eliminate expression of TAGL
 CC genes for certain applications. TAGL enzymes may also be useful for the
 CC processing of plant seed oils and for the development of novel seed
 CC oils. The TAGL enzymes can also be used as targets to facilitate the
 CC design and/or identification of inhibitors of those enzymes that may be
 CC useful as herbicides. This is desirable because inhibition of the
 CC activity of either of the enzymes could lead to an inhibition of plant
 CC growth.
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 SQ
 Query Match 60.38; Score 35; DB 21; Length 246;
 Best Local Similarity 62.58; Pred. No. 46;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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 Db 75 ILPTIME 82
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 XX 17-OCT-2000 (first entry)
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 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
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KW termination sequence.
 XX Arabidopsis thaliana.
 OS
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 PN
 XX 06-SEP-2000.
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 XX 25-FEB-2000; 2000EP-0301439.
 PF
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Query Match 60.3%; Score 35; DB 21; Length 251;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMMF 10
Db 195 RQLVPTKLF 204
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XX
AC AAG61262;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79442.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PR	23-MAR-1999;	99US-0125788.	99US-0142977.
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PR	24-JUN-1999;	99US-0140695.	99US-0150884.
PR	28-JUN-1999;	99US-0140823.	99US-0151065.
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PR	30-JUN-1999;	99US-0141287.	99US-0151080.
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PR	01-JUL-1999;	99US-0142154.	99US-0151438.
PR	02-JUL-1999;	99US-0142055.	99US-0151930.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 251;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVPTMMF 10
Db 195 RQLVPTKLF 204

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AAG09306
ID AAG09306 standard; Protein; 252 AA.

XX AC AAG09306;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 7186.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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PR 07-SEP-1999; 99US-0152363.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.

PR 08-OCT-1999; 99US-0158232.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 252;
Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVPTMMF 10
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Db 196 RQLVPTKLF 205

RESULT 14

AAG09305
ID AAG09305 standard; Protein; 254 AA.

XX AC AAG09305;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 7185.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 07-OCT-1999; 99US-0158029.
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 PR 28-OCT-1999; 99US-0161992.
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Query Match 60.3%; Score 35; DB 21; Length 254;
 Best Local Similarity 60.0%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
 | : |||| : |
 Db 198 RQLVPTKLF 207

RESULT 15
 AAB86353
 ID AAB86353 standard; Protein; 254 AA.

XX AC AAB86353;
 DT 20-SEP-2001 (first entry)
 XX A. thaliana allene oxide cyclase protein SEQ ID 10.

XX Allene oxide cyclase; jasmonic acid; plant; AOC; jasmonate biosynthesis;
 KW signalling molecule; gene expression; stress response; perfume synthesis;
 KW wound-induced signal cascade; defensive response; transgenic plant;
 KW protease inhibitor synthesis; phytoalexin synthesis; alkaloid synthesis;
 KW pathogen resistance; herbicide resistance; ultra-violet protection;
 KW secondary metabolite production; male sterility; flower development;
 KW seed formation; germination.

XX Arabidopsis thaliana.

OS WO200157224-A2.

PN 09-AUG-2001.

PD 02-FEB-2001; 2001WO-EP01148.

PF 02-FEB-2000; 2000DE-1004468.

PR (PFLA-) INST PFLANZENBIOCHEMIE.

PA Ziegler J, Stenzel I, Hause B, Wasternack C;

PI WPI; 2001-483438/52.

XX N-PSDB; AAH21490.

XX Nucleic acid encoding plant allene oxide cyclase, useful for producing
 PT transgenic plants with altered jasmonic acid synthesis, e.g. increased
 PT resistance to pathogens -

XX Claim 1b; Page 55-56; 66pp; German.

XX This invention describes novel nucleic acids (I), encoding proteins
 CC (II) with the activity of the allene oxide cyclase (AOC) involved in
 CC jasmonate biosynthesis. Jasmonic acid (JA) is a signalling molecule
 CC involved in: (i) altered gene expression in plants in response to
 CC stress; and (ii) developmental processes. It is also an intermediate in
 CC the wound-induced signal cascade and induces many defensive responses in
 CC plants, including synthesis of protease inhibitors, phytoalexins,
 CC alkaloids and perfumes. (I) is used: (i) to produce transgenic plants,
 CC cells etc. with altered AOC activity, specifically altered resistance to
 CC pathogens and herbivores, optimal plant/usable insect/pest interaction;
 CC increased biomass, altered carbohydrate and nitrogen metabolism;
 CC increased production of secondary metabolites (especially alkaloids
 CC and/or phytoalexins), optimal ultra-violet protection; altered male
 CC sterility and/or altered development, especially flower development, seed
 CC formation and/or germination; (ii) for selective production of 9S/13S
 CC (cis(+)-12-oxophytodienoic acid (13), a precursor of jasmonic acid
 CC (JA); (iii) for isolation of homologous sequences; and (iv) to express
 CC AOC in prokaryotic or eukaryotic cells or (in antisense orientation) to
 CC inhibit its expression. (I) Makes possible large scale production of high
 CC purity JA. (I) is very specific for production of (III) (contrast
 CC non-enzymatic methods which produce mixtures of isomers) which is a
 CC precursor for the natural enantiomer of JA. This sequence represents the
 CC Arabidopsis thaliana AOC described in the invention.

XX Sequence 254 AA;

Query Match 60.3%; Score 35; DB 22; Length 254;
 Best Local Similarity 60.0%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
 | : |||| : |
 Db 198 RQLVPTKLF 207

RESULT 16
 ABB90980
 ID ABB90980 standard; Protein; 254 AA.

XX AC ABB90980;

XX 31-MAY-2002 (first entry)

XX Herbicidally active polypeptide SEQ ID NO 191.

XX Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP09892.

XX 28-AUG-2001; 2001WO-EP09892.

XX (FARB) BAYER AG.

XX Tietjen K, Weidner M;

XX WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms -

XX Claim 5; SEQ ID NO 191; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins

CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
XX useful as herbicides.

XX SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 23; Length 254;
Best Local Similarity 60.08; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVPTMFM 10
I :||||:|
Db 198 RQLVPTKLF 207

RESULT 17

AAG07359
ID AAG07359 standard; Protein; 258 AA.

XX AC AAG07359;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 4483.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123348.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 08-APR-1999; 99US-0128714.
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PR 28-APR-1999; 99US-0130891.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 06-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
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PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred. NO. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
DB 202 RQLVYPTKLF 211
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RESULT 18
AAG61261
ID AAG61261 standard; Protein; 258 AA.
XX
AC AAG61261;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79441.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 06-APR-1999; 99US-0128234.
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Query Match 58.6%; Score 34; DB 21; Length 56;
Best Local Similarity 45.5%; Pred. No. 14;
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DT 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
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KW termination sequence.
XX Arabidopsis thaliana.
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Query Match 58.6%; Score 34; DB 21; Length 57;
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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Query Match 58.6%; Score 34; DB 21; Length 57;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 3; Indels

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17-OCT-2000 (first entry)

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KW hybridisation assay; genetic mapping; gene expression control; promoter
KW termination sequence.

OS *Arabidopsis thaliana*.

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Query Match 58.6%; Score 34; DB 21; Length 264;
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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Query Match 58.6%; Score 34; DB 21; Length 264;
Best Local Similarity 75.0%; Pred.No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
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OS Homo sapiens.
XX
PN WO200157190-A2.
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PD 09-AUG-2001.
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PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
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PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI; 2001-476283/51.
 DR N-PSDB; AAK51462.
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 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 XX Claim 20; Page 3215-3216; 6221pp; English.
 XX
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
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 Db 97 ILYPVMMF 104

Search completed: July 16, 2003, 14:33:11
 Job time : 49.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:31:07 ; Search time 15 Seconds
(without alignments)
21.577 Million cell updates/sec

Title: US-09-923-716c-1
Perfect score: 58
Sequence: 1 RTVVPTMFK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 75 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	38	65.5	262	US-08-634-475-2	Sequence 2, Appli
4	38	65.5	262	US-09-709-791-2	Sequence 2, Appli
5	34	58.6	591	US-09-352-159-46	Sequence 46, Appli
6	34	58.6	598	US-09-352-159-42	Sequence 42, Appli
7	33	56.9	700	US-08-274-121B-5	Sequence 5, Appli
8	32	55.2	462	US-09-352-159-6	Sequence 6, Appli
9	32	55.2	462	US-09-352-159-8	Sequence 8, Appli
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37	55.2	1196	4	US-09-352-159-31	Sequence 31, Appli
38	55.2	1196	4	US-09-352-168-31	Sequence 31, Appli
39	55.2	1205	4	US-09-352-159-29	Sequence 29, Appli
40	55.2	1205	4	US-09-352-168-29	Sequence 29, Appli
41	53.4	125	2	US-08-408-095-35	Sequence 35, Appli
42	53.4	149	4	US-09-134-001C-2957	Sequence 2957, Ap
43	53.4	201	2	US-08-933-750C-21	Sequence 21, Appli
44	53.4	201	4	US-09-234-613-21	Sequence 21, Appli
45	53.4	320	2	US-08-933-750C-12	Sequence 12, Appli
46	53.4	320	4	US-09-234-613-12	Sequence 12, Appli
47	53.4	535	4	US-09-269-731-4	Sequence 4, Appli
48	53.4	1487	2	US-08-760-489-2	Sequence 2, Appli
49	53.4	1487	2	US-08-760-489-4	Sequence 4, Appli
50	53.4	1487	4	US-09-185-373-2	Sequence 2, Appli
51	53.4	1487	4	US-09-185-373-4	Sequence 4, Appli
52	53.4	3011	3	US-08-811-566-20	Sequence 20, Appli
53	53.4	3011	4	US-09-014-416-1	Sequence 1, Appli
54	53.4	3011	4	US-09-014-416-5	Sequence 5, Appli
55	53.4	3011	4	US-09-034-756-20	Sequence 20, Appli
56	53.4	3012	3	US-08-811-566-2	Sequence 2, Appli
57	53.4	3012	4	US-09-034-756-2	Sequence 2, Appli
58	52.6	371	4	US-09-574-141A-56	Sequence 56, Appli
59	30.5	280	6	5182210-12	Patent No. 5182210
60	51.7	451	1	US-08-625-322-4	Sequence 4, Appli
61	51.7	490	2	US-08-673-789-13	Sequence 13, Appli
62	51.7	621	3	US-08-604-789B-4	Sequence 4, Appli
63	51.7	621	4	US-09-312-721A-4	Sequence 4, Appli
64	51.7	697	2	US-08-674-351-4	Sequence 4, Appli
65	51.7	701	4	US-09-132-028-2	Sequence 2, Appli
66	51.7	722	4	US-09-134-001C-5482	Sequence 5482, Ap
67	51.7	744	1	US-08-162-809-20	Sequence 20, Appli
68	51.7	1437	3	US-09-061-400-2	Sequence 2, Appli
69	51.7	1453	2	US-09-001-273-2	Sequence 2, Appli
70	51.7	1453	4	US-08-843-459A-2	Sequence 2, Appli
71	29	50.0	17	US-09-227-357-426	Sequence 426, App
72	29	50.0	68	US-09-097-889-17	Sequence 17, Appli
73	29	50.0	156	US-09-134-001C-4450	Sequence 4450, Ap
74	29	50.0	305	US-08-858-207A-392	Sequence 392, App
75	29	50.0	401	US-09-134-001C-4403	Sequence 4403, Ap

ALIGNMENTS

RESULT 1
US-08-634-475-3
; Sequence 3, Application US/08634475
; Patent No. 6143950
; GENERAL INFORMATION:
; APPLICANT: Chory et al., Joanne
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
; TITLE OF INVENTION: DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/634,475
;; APPLICATION NUMBER: US/08/634,475
;; FILING DATE: 18-APR-1996
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07251/015001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619/678-5070
;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 246 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-634-475-3

Query Match 65.5%; Score 38; DB 4; Length 246;
Best Local Similarity 45.5%; Pred. No. 8.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
Db 77 RTIYPLRLFR 87

RESULT 2
US-09-709-791-3
; Sequence 3, Application US/09709791
; Patent No. 6352846
; GENERAL INFORMATION:
; APPLICANT: Chory, Joanne
; Li, Jianming
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,791
; FILING DATE: 07-NOV-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: SALKINS.010DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/235-8550
; TELEFAX: 619/235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-709-791-3

Query Match 65.5%; Score 38; DB 4; Length 246;
Best Local Similarity 45.5%; Pred. No. 8.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
Db 77 RTIYPLRLFR 87

RESULT 3
US-08-634-475-2
; Sequence 2, Application US/08634475
; Patent No. 6143950
; GENERAL INFORMATION:
; APPLICANT: Chory et al., Joanne
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
DET2
; TITLE OF INVENTION: DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,475
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07251/015001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-634-475-2

Query Match 65.5%; Score 38; DB 4; Length 262;
Best Local Similarity 45.5%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
Db 93 RTIYPLRLFR 103

RESULT 4
US-09-709-791-2
; Sequence 2, Application US/09709791
; Patent No. 6352846
; GENERAL INFORMATION:
; APPLICANT: Chory, Joanne
; Li, Jianming
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th floor
; CITY: Newport Beach

STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-NOV-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: SALKINS.010DV1
TELEPHONE: 619/235-8550
TELEFAX: 619/235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-791-2

Query Match 65.5%; Score 38; DB 4; Length 262;
Best Local Similarity 45.5%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
|:|:|:|:|:
Db 93 RTIYPLRLFR 103

RESULT 5
US-09-352-159-46
; Sequence 46, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rhinocycladiella atrovirens
US-09-352-159-46

Query Match 58.6%; Score 34; DB 4; Length 591;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|:|:
Db 405 TTYLPTLIF 413

RESULT 6

US-09-352-159-42
; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Rhinocycladiella atrovirens
US-09-352-159-42

Query Match 58.6%; Score 34; DB 4; Length 598;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|:|:
Db 406 TTYLPTLIF 414

RESULT 7
US-08-274-121B-5
; Sequence 5, Application US/08274121B
; Patent No. 6133034
; GENERAL INFORMATION:
; APPLICANT: Arne Reider Strom
; APPLICANT: Inga Kaasen
; APPLICANT: Olaf Bay Styrvold
; APPLICANT: John McDougall
; TITLE OF INVENTION: Methods and Compositions
; TITLE OF INVENTION: Related To The Production
; TITLE OF INVENTION: of Trehalose
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,121B
; FILING DATE: 12-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/893,099
; FILING DATE: 27-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 86(1)
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-274-121B-5

Query Match 56.9%; Score 33; DB 4; Length 700;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
| :||| |
Db 672 KAIYPTFFF 681

RESULT 8

US-09-352-159-6
; Sequence 6, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-6

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :||| |
Db 270 TTLYPTLTF 278

RESULT 9

US-09-352-159-8
; Sequence 8, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8

; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-8

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :||| |
Db 270 TTLYPTLTF 278

RESULT 10

US-09-352-168-6
; Sequence 6, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-6

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :||| |
Db 270 TTLYPTLTF 278

RESULT 11

US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-8


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Query Match      55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
DB      270 TTLPTLTF 278

RESULT 12
US-09-352-159-11
; Sequence 11, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352.159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092.936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135.391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-11

Query Match      55.2%; Score 32; DB 4; Length 463;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
DB      271 TTLPTLTF 279

RESULT 13
US-09-352-168-11
; Sequence 11, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duivick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352.168A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092.936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; OTHER INFORMATION: Extra lysine in the polypeptide sequence of
; OTHER INFORMATION: K:trpAO, 463 aa.
US-09-352-168-11

Query Match      55.2%; Score 32; DB 4; Length 463;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
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Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
DB      271 TTLPTLTF 279

RESULT 14
US-08-959-011-3
; Sequence 3, Application US/08959011
; Patent No. 5932444
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959.011
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0412 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 497984
US-08-959-011-3

Query Match      55.2%; Score 32; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RTVVYPTM 8
DB      244 RTVVPTM 251

RESULT 15
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
```

```
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-09-352-159-21

Query Match          55.2%; Score 32; DB 4; Length 487;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
Db      295 TTLYPTLTF 303

RESULT 16
US-09-352-168-21
; Sequence 21, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-352-168-21

Query Match          55.2%; Score 32; DB 4; Length 487;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
Db      295 TTLYPTLTF 303

RESULT 17
US-09-001-826-23
; Sequence 23, Application US/09001826A
; Patent No. 5965727
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: SONG, HEE-SOOK
; APPLICANT: BROTHERTON, JEFFREY E.
; APPLICANT: WIDHOLM, JACK M.
; TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: U1001.C1
; CURRENT APPLICATION NUMBER: US/09/001,826A
; CURRENT FILING DATE: 1997-12-31
; EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
; EARLIER FILING DATE: 1997-07-25; 1996-07-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO 23
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-001-826-23

Query Match          55.2%; Score 32; DB 2; Length 491;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVVVYPT 7
Db      422 RTIVFPT 428

RESULT 18
US-09-352-159-17
; Sequence 17, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
US-09-352-159-17

Query Match          55.2%; Score 32; DB 4; Length 554;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
Db      362 TTLYPTLTF 370

RESULT 19
US-09-352-168-17
; Sequence 17, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
```

APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 554
TYPE: PRT
ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(89)
OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-352-168-17

Query Match 55.2%; Score 32; DB 4; Length 554;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 362 TTYLPTLTF 370

RESULT 20
US-09-486-382B-2
Sequence 2, Application US/09486382B
Patent No. 6388174
GENERAL INFORMATION:
APPLICANT: Hokko Chemical Industry Co., Ltd.
TITLE OF INVENTION: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
FILE REFERENCE: 10647
CURRENT APPLICATION NUMBER: US/09/486,382B
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: JP 9-235049
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 577
TYPE: PRT
ORGANISM: Oryza sativa
US-09-486-382B-2

Query Match 55.2%; Score 32; DB 4; Length 577;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
| :||: |
Db 508 RTIVPT 514

RESULT 21
US-09-486-382B-13
Sequence 13, Application US/09486382B
Patent No. 6388174
GENERAL INFORMATION:
APPLICANT: Hokko Chemical Industry Co., Ltd.
TITLE OF INVENTION: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
FILE REFERENCE: 10647
CURRENT APPLICATION NUMBER: US/09/486,382B
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: JP 9-235049

PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 577
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Modified amino acid sequence of Sequence No. 6388174
Patent No. 6388174
US-09-486-382B-13

Query Match 55.2%; Score 32; DB 4; Length 577;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
| :||: |
Db 508 RTIVPT 514

RESULT 22
US-08-604-789B-3
Sequence 3, Application US/08604789B
Patent No. 6118047
GENERAL INFORMATION:
APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
Kriz, A.L.
TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
OVERPRODUCTION
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,789B
FILING DATE: 19-Jan-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
TELEFAX: (612) 339-3061
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-08-604-789B-3
Query Match 55.2%; Score 32; DB 3; Length 595;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RTVVYPT 7
      ||:|:|
Db      526 RTIVFPT 532

RESULT 23
US-09-312-721A-3
; Sequence 3, Application US/09312721A
; Patent No. 6271016
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312.721A
; FILING DATE: 17-May-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,789
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.0260US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-312-721A-3

Query Match      55.2%; Score 32; DB 4; Length 595;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVVYPT 7
      ||:|:|
Db      526 RTIVFPT 532

RESULT 24
US-09-352-159-40
; Sequence 40, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
```

```
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352.159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (216)...(216)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-352-159-40
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Query Match      55.2%; Score 32; DB 4; Length 598;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      2 TVVYPTMMF 10
      |:|:|:|
Db      406 TTLYPTLTF 414
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RESULT 25
US-09-352-159-23
; Sequence 23, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352.159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; US-09-352-159-23
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Query Match      55.2%; Score 32; DB 4; Length 600;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      2 TVVYPTMMF 10
      |:|:|:|
Db      408 TTLYPTLTF 416
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Search completed: July 16, 2003, 14:38:03
Job time : 22 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:33:19 ; Search time 27.6667 Seconds
(without alignments)
47.218 Million cell updates/sec

Title: US-09-923-716c-1
Perfect score: 58
Sequence: 1 RTVVPTMFKE 11

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	58.6	322	9	US-10-183-116-16
2	34	58.6	322	9	US-10-079-384-4
3	34	58.6	600	9	US-10-072-307-28
4	34	58.6	600	9	US-10-072-307-30
5	34	58.6	600	9	US-10-072-307-35
6	34	58.6	600	9	US-10-072-307-37
7	34	58.6	600	9	US-10-072-307-40
8	34	58.6	600	9	US-10-072-307-43
9	34	58.6	600	9	US-10-072-307-60
10	34	58.6	600	9	US-10-072-307-64
11	33	56.9	600	9	US-10-072-307-62
12	33	56.9	656	9	US-09-738-626-4577
13	32	55.2	447	9	US-10-169-048-34
14	32	55.2	447	9	US-10-169-048-44
15	32	55.2	462	9	US-09-770-564-6
16	32	55.2	462	9	US-09-770-564-8
17	32	55.2	463	9	US-10-072-307-46
18	32	55.2	463	9	US-10-072-307-47
19	32	55.2	463	9	US-10-072-307-48

20	32	55.2	463	9	US-10-072-307-50
21	32	55.2	463	9	US-09-770-564-11
22	32	55.2	487	9	US-09-770-564-21
23	32	55.2	539	9	US-10-072-307-34
24	32	55.2	554	9	US-09-770-564-17
25	32	55.2	595	10	US-09-733-300-3
26	32	55.2	600	9	US-10-072-307-26
27	32	55.2	600	9	US-10-072-307-27
28	32	55.2	600	9	US-10-072-307-29
29	32	55.2	600	9	US-10-072-307-31
30	32	55.2	600	9	US-10-072-307-32
31	32	55.2	600	9	US-10-072-307-33
32	32	55.2	600	9	US-10-072-307-36
33	32	55.2	600	9	US-10-072-307-38
34	32	55.2	600	9	US-10-072-307-41
35	32	55.2	600	9	US-10-072-307-42
36	32	55.2	600	9	US-10-072-307-44
37	32	55.2	600	9	US-10-072-307-45
38	32	55.2	600	9	US-10-072-307-52
39	32	55.2	600	9	US-10-072-307-54
40	32	55.2	600	9	US-10-072-307-56
41	32	55.2	600	9	US-10-072-307-58
42	32	55.2	600	9	US-10-072-307-66
43	32	55.2	600	9	US-09-770-564-23
44	32	55.2	692	9	US-09-770-564-19
45	32	55.2	829	9	US-09-770-564-33
46	32	55.2	991	9	US-09-770-564-27
47	32	55.2	1000	9	US-09-770-564-25
48	32	55.2	1196	9	US-09-770-564-31
49	32	55.2	1205	9	US-09-770-564-29
50	31	53.4	57	10	US-09-864-761-47860
51	31	53.4	58	9	US-09-764-891-2918
52	31	53.4	157	9	US-09-992-598-103
53	31	53.4	157	9	US-09-989-293A-103
54	31	53.4	157	9	US-09-989-735-103
55	31	53.4	157	9	US-09-990-444-103
56	31	53.4	157	9	US-09-989-730-103
57	31	53.4	157	9	US-09-991-181-103
58	31	53.4	157	9	US-09-993-687-103
59	31	53.4	157	9	US-09-989-734-103
60	31	53.4	157	9	US-09-993-667-103
61	31	53.4	157	9	US-09-997-653-103
62	31	53.4	157	9	US-10-174-590-90
63	31	53.4	157	9	US-10-176-758-90
64	31	53.4	157	9	US-10-175-737-90
65	31	53.4	157	9	US-09-993-667-103
66	31	53.4	157	9	US-10-173-706-90
67	31	53.4	157	9	US-10-175-738-90
68	31	53.4	157	9	US-10-175-752-90
69	31	53.4	157	9	US-10-176-482-90
70	31	53.4	157	9	US-10-176-757-90
71	31	53.4	157	9	US-10-176-913-90
72	31	53.4	157	9	US-10-180-552-90
73	31	53.4	157	9	US-10-180-557-90
74	31	53.4	157	9	US-09-990-438-103
75	31	53.4	157	9	US-09-990-562-103

ALIGNMENTS

RESULT 1
US-10-183-116-16
; Sequence 16, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CP1

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; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-16
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Query Match          58.6%; Score 34; DB 9; Length 322;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      3 VVYPTMMF 10
DB      97 ILYPVMMF 104
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RESULT 2

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US-10-079-384-4
; Sequence 4, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-4
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Query Match          58.6%; Score 34; DB 9; Length 322;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      3 VVYPTMMF 10
DB      97 ILYPVMMF 104
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RESULT 3

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US-10-072-307-28
; Sequence 28, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
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; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 28
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_F7
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-28
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Query Match          58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY      2 TVVYPTMMF 10
DB      408 TTYLPTLIF 416
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RESULT 4

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US-10-072-307-30
; Sequence 30, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 30
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G11
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-30
```

```
Query Match          58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 TVVYPTMMF 10
DB      408 TTYLPTLIF 416
```

RESULT 5

```
US-10-072-307-35
; Sequence 35, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
```

; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 35

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: LIMS-SeqID Translation_of_4F15C3

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-072-307-35

Query Match

Best Local Similarity 58.6%; Score 34; DB 9; Length 600;

Matches 5; Conservative 3; Mismatches 1; Indels 0;

QY 2 TVVYPTMMF 10

Db 408 TLYPTLIF 416

1:||||:1

RESULT 6

US-10-072-307-37

; Sequence 37, Application US/10072307

; Publication No. US20030056245A1

; GENERAL INFORMATION:

; APPLICANT: Chatterjee, Ranjini

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: English, James

; TITLE OF INVENTION: API Amine Oxidase Variants

; FILE REFERENCE: 02-10402US

; CURRENT APPLICATION NUMBER: US/10/072,307

; CURRENT FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: US 60/266,918

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: US 60/300,324

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 37

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: LIMS-SeqID Translation_of_4F19F2

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-072-307-37

Query Match

Best Local Similarity 58.6%; Score 34; DB 9; Length 600;

Matches 5; Conservative 3; Mismatches 1; Indels 0;

QY 2 TVVYPTMMF 10

Db 408 TLYPTLIF 416

1:||||:1

RESULT 7

US-10-072-307-40

; Sequence 40, Application US/10072307

; Publication No. US20030056245A1

; GENERAL INFORMATION:

; APPLICANT: Chatterjee, Ranjini

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: English, James

; TITLE OF INVENTION: API Amine Oxidase Variants

; FILE REFERENCE: 02-10402US

; CURRENT APPLICATION NUMBER: US/10/072,307

; CURRENT FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: US 60/266,918

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: US 60/300,324

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 40

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: LIMS-SeqID Translation_of_4F24F2

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-072-307-40

Query Match

Best Local Similarity 58.6%; Score 34; DB 9; Length 600;

Matches 5; Conservative 3; Mismatches 1; Indels 0;

QY 2 TVVYPTMMF 10

Db 408 TLYPTLIF 416

1:||||:1

RESULT 8

US-10-072-307-43

; Sequence 43, Application US/10072307

; Publication No. US20030056245A1

; GENERAL INFORMATION:

; APPLICANT: Chatterjee, Ranjini

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: English, James

; TITLE OF INVENTION: API Amine Oxidase Variants

; FILE REFERENCE: 02-10402US

; CURRENT APPLICATION NUMBER: US/10/072,307

; CURRENT FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: US 60/266,918

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: US 60/300,324

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 43

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: LIMS-SeqID Translation_of_4F3B5

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-072-307-43

Query Match

Best Local Similarity 58.6%; Score 34; DB 9; Length 600;

Matches 5; Conservative 3; Mismatches 1; Indels 0;

QY 2 TVVYPTMMF 10

Db 408 TLYPTLIF 416

1:||||:1

RESULT 9

US-10-072-307-60

; Sequence 60, Application US/10072307

; Publication No. US20030056245A1

; GENERAL INFORMATION:

; APPLICANT: Chatterjee, Ranjini

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: English, James

; TITLE OF INVENTION: API Amine Oxidase Variants

; FILE REFERENCE: 02-10402US

; CURRENT APPLICATION NUMBER: US/10/072,307

; CURRENT FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: US 60/266,918

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: US 60/300,324

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 60

```
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocliadiella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 215
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 216
; OTHER INFORMATION: Xaa = Gln, His
US-10-072-307-60

Query Match          58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TVVYPTMMF 10
Db      408 TTYLPTLIF 416

RESULT 10
US-10-072-307-64
; Sequence 64, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocliadiella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 13
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 403
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 404
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 419
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 433
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 443
; OTHER INFORMATION: Xaa = Ter, Cys, Trp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 478
; OTHER INFORMATION: Xaa = Leu, Ter, Ser, Trp
; FEATURE:
; NAME/KEY: unsure

; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocliadiella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 538
; OTHER INFORMATION: Xaa = Ter, Arg, Gly
US-10-072-307-64

Query Match          58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TVVYPTMMF 10
Db      408 TTYLPTLIF 416

RESULT 11
US-10-072-307-62
; Sequence 62, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocliadiella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 187
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 209
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 244
; OTHER INFORMATION: Xaa = Glu, Asp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 262
; OTHER INFORMATION: Xaa = Ter, Cys, Trp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 295
; OTHER INFORMATION: Xaa = Tyr, Asn, Asp, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 299
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 403
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 405
; OTHER INFORMATION: Xaa = Ala, Thr, Pro, Ser
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 409
```


; OTHER INFORMATION: Xaa = Ala, Thr, Ser, Pro
US-10-072-307-62

Query Match 56.9%; Score 33; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
I :|||:
Db 408 TXLYPTLIF 416

RESULT 12

US-09-738-626-4577
; Sequence 4577, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIRO

; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO

; APPLICANT: TATEISHI, NAOKO

; APPLICANT: SENOH, AKIHIRO

; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 7059

; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 4577

; LENGTH: 656

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-4577

Query Match 56.9%; Score 33; DB 9; Length 656;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMF 10
I :|||:
Db 307 IIMPTMMF 314

RESULT 13

US-10-169-048-34

; Sequence 34, Application US/10169048

; Publication No. US20030072769A1

; GENERAL INFORMATION:

; APPLICANT: Clarke, Edna Elizabeth

; APPLICANT: Zhou, Liqing

; APPLICANT: Shea, Jacqueline Elizabeth

; APPLICANT: Feldman, Robert Graham

; APPLICANT: Holden, David William

; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use

; FILE REFERENCE: GJE-97

; CURRENT APPLICATION NUMBER: US/10/169,048

; CURRENT FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: PCT/GB00/04997

; PRIOR FILING DATE: 2000-12-22

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 34

; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-34

Query Match 55.2%; Score 32; DB 9; Length 447;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
I :|||:
Db 190 QTMYPTEFFK 200

RESULT 14

US-10-169-048-44

; Sequence 44, Application US/10169048

; Publication No. US20030072769A1

; GENERAL INFORMATION:

; APPLICANT: Clarke, Edna Elizabeth

; APPLICANT: Zhou, Liqing

; APPLICANT: Shea, Jacqueline Elizabeth

; APPLICANT: Feldman, Robert Graham

; APPLICANT: Holden, David William

; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their

; FILE REFERENCE: GJE-97

; CURRENT APPLICATION NUMBER: US/10/169,048

; CURRENT FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: PCT/GB00/04997

; PRIOR FILING DATE: 2000-12-22

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 44

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Streptococcus pyogenes

US-10-169-048-44

Query Match 55.2%; Score 32; DB 9; Length 447;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
I :|||:
Db 190 QTMYPTEFFK 200

RESULT 15

US-09-770-564-6

; Sequence 6, Application US/09770564

; Publication No. US20030126636A1

; GENERAL INFORMATION:

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: Folkerts, Otto

; APPLICANT: Gilliam, Jacob T.

; APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; FILE REFERENCE: 0875

; CURRENT APPLICATION NUMBER: US/09/770,564

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 09/352,168

; PRIOR FILING DATE: 1999-07-12

; PRIOR APPLICATION NUMBER: 60/092,936

; PRIOR FILING DATE: 1998-07-25

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Exophiala spinifera

US-09-770-564-6

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 270 TTLYPTLTF 278

RESULT 16

US-09-770-564-8
; Sequence 8, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 1999-07-12
; PRIOR FILING DATE: 1998-07-25
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-770-564-8

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 270 TTLYPTLTF 278

RESULT 17

US-10-072-307-46
; Sequence 46, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 46
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_TrHI
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-46

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 271 TTLYPTLTF 279

RESULT 18

US-10-072-307-47
; Sequence 47, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 47
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G6
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-47

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 271 TTLYPTLTF 279

RESULT 19

US-10-072-307-48
; Sequence 48, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 48
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_H8
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-48

Query Match 55.2%; Score 32; DB 9; Length 463;

Best Local Similarity 55.6%; Pred. NO. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTLXPTLTF 279

RESULT 20

US-10-072-307-50
; Sequence 50, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APL Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 50
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_B6
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-50

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. NO. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTLXPTLTF 279

RESULT 21

US-09-770-564-11
; Sequence 11, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; OTHER INFORMATION: Extra lysine in the polypeptide sequence of
; OTHER INFORMATION: K:TRAPAO, 463 aa.
US-09-770-564-11

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. NO. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTLXPTLTF 279

RESULT 22

US-09-770-564-21
; Sequence 21, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:TRAPAO translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature TRAPAO in maize.
US-09-770-564-21

Query Match 55.2%; Score 32; DB 9; Length 487;
Best Local Similarity 55.6%; Pred. NO. 3.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 295 TTLXPTLTF 303

RESULT 23

US-10-072-307-34
; Sequence 34, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APL Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 34
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Artificial Sequence

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 20 Seconds
(without alignments)
52.874 Million cell updates/sec

Title: US-09-923-716c-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	333	2 S74406	hypothetical prote
2	41	70.7	974	2 T29545	hypothetical prote
3	38	65.5	262	2 C84800	3-oxo-5-alpha-ster
4	38	65.5	394	2 G86657	ABC transporter At
5	37	63.8	395	2 H83424	hypothetical prote
6	35	60.3	180	2 D86267	T6J4.4 protein - A
7	35	60.3	435	2 E72342	pmbA-related prote
8	35	60.3	598	2 AG0890	probable arylsulfa
9	35	60.3	887	2 B96598	hypothetical prote
10	34	58.6	303	2 H84758	hypothetical prote
11	34	58.6	347	2 AD3513	channel protein vi
12	34	58.6	373	2 S17955	long-chain-fatty-a
13	34	58.6	373	2 S15161	long-chain-fatty-a
14	34	58.6	389	2 AD0478	acetylornithine de
15	34	58.6	404	2 B41317	O-antigen ligase c
16	34	58.6	404	2 AE0973	O-antigen ligase l
17	34	58.6	464	2 T50785	nucleoid DNA-bind
18	34	58.6	674	2 D72329	hypothetical prote
19	34	58.6	711	2 A86424	unknown protein, 3
20	33	57.8	1724	2 T13942	UNC-13-B protein -
21	33	56.9	120	1 E69798	conserved hypothet
22	33	56.9	136	2 AG0710	regulator of nucle
23	33	56.9	136	2 E85560	regulator of nucle
24	33	56.9	136	2 I57917	nucleoside diphosp
25	33	56.9	205	2 S29308	hypothetical prote
26	33	56.9	205	2 F83013	probable transcrip
27	33	56.9	221	2 AH0324	probable transport
28	33	56.9	261	2 T05447	hypothetical prote
29	33	56.9	390	2 AF3425	oxidoreductase (EC

30	56.9	394	2 S69870	hypothetical prote
31	56.9	531	2 D90453	hypothetical prote
32	56.9	551	2 D69282	glutamyl-tRNA synt
33	56.9	594	2 S00961	hypothetical prote
34	56.9	821	2 B75530	ATP-dependent prot
35	56.9	1021	2 T08601	hypothetical prote
36	56.9	1235	2 AC1358	ATP-dependent deox
37	56.9	1235	2 AC1728	ATP-dependent deox
38	55.2	61	1 F2RZKS	photosystem II pro
39	55.2	136	2 AC0578	regulator of nucle
40	55.2	142	2 G98072	7,8-dihydro-8-oxog
41	55.2	143	1 WMBE6H	transcription regu
42	55.2	143	2 T43976	transactivator [im
43	55.2	169	2 S72166	lipopolysaccharide
44	55.2	201	2 T07011	proteinase inhibit
45	55.2	203	2 E75413	conserved hypothet
46	55.2	214	2 G71318	hypothetical prote
47	55.2	214	2 D89985	hypothetical prote
48	55.2	214	2 T49174	hypothetical prote
49	55.2	283	2 T13879	maturase-like prot
50	55.2	283	2 AG1560	hypothetical prote
51	55.2	283	2 A11202	hypothetical prote
52	55.2	285	2 T09308	immediate-early pr
53	55.2	334	2 T44163	hypothetical prote
54	55.2	421	2 S26246	glutamate/aspartat
55	55.2	458	2 A96938	polyA polymerase I
56	55.2	468	2 A55116	vacuolar ATPase [E
57	55.2	513	2 T40998	hypothetical prote
58	55.2	526	2 T49199	anthranilate synth
59	55.2	543	2 T22585	hypothetical prote
60	55.2	564	2 S15962	hypothetical prote
61	55.2	595	2 JQ1684	anthranilate synth
62	55.2	603	2 T11843	NADH2 dehydrogenas
63	55.2	620	2 T21391	hypothetical prote
64	55.2	1416	2 D71350	probable DNA-direc
65	55.2	1501	2 T29094	ribose-bisphosph
66	55.2	1716	2 T14103	probable DNA-direc
67	55.2	3175	1 RRWVEV	genome polyprotein
68	53.4	80	2 A60450	hypothetical prote
69	53.4	95	2 B83814	Na+/H+ antiporter
70	53.4	104	2 T17649	hypothetical prote
71	53.4	105	2 T44098	hypothetical prote
72	53.4	142	2 G95207	MutT/nudix family
73	53.4	185	2 T29063	hypothetical prote
74	53.4	207	2 D65095	hypothetical prote
75	53.4	207	2 A98123	hypothetical prote

ALIGNMENTS

RESULT 1

S74406
hypothetical protein sll0456 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74406
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yae, DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74406
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-333 <KAN>
A:Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10324.1; PID:d101
A>Note: the nucleotide sequence was submitted to the EMBL data Library, June 1996

Query Match 70.7%; Score 41; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 2.8;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|||||::|
Db 172 TVVYPTLVF 180

RESULT 2

T29545

hypothetical protein F48C1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29545

R:Gattung, S.; Le, T.T.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid F48C1.

A:Reference number: Z20638

A:Accession: T29545

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-974 <GAT>

A:Cross-references: EMBL:U97015; PIDN:AA52345.1; GSPDB:GN00019; CESP:F48C1.1

A:Experimental source: strain Bristol N2; clone F48C1

C:Genetics:

A:Gene: CESP:F48C1.1

A:Map position: 1

A:Introns: 15/2; 58/3; 110/3; 150/1; 176/1; 267/2; 296/2; 326/2; 394/3; 441/1; 550/3; 59

Query Match 70.7%; Score 41; DB 2; Length 974;

Best Local Similarity 60.0%; Pred. No. 8.3;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10

:|::||| |||

Db 851 QTIYPPMMF 860

RESULT 3

C84800

3-oxo-5-alpha-steroid 4-dehydrogenase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: C84800

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84800

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-262 <STO>

A:Cross-references: GB:AE002093; NID:g4895180; PIDN:AAD32767.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g38050

A:Map position: 2

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match 65.5%; Score 38; DB 2; Length 262;

Best Local Similarity 45.5%; Pred. No. 8.2;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 11

:|::||| ::|

Db 93 RTIYPLRLR 103

RESULT 4

G8657

ABC transporter ATP binding protein ycgB [imported] - Lactococcus lactis subsp. lactis

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: G8657

R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh

Genome Res. 11, 731-753, 2001

A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G8657

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <STO>

A:Cross-references: GB:AE005176; PID:g12723123; PIDN:AAK04361.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: ycgB

Query Match 65.5%; Score 38; DB 2; Length 394;

Best Local Similarity 66.7%; Pred. No. 12;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10

:|::||| |

Db 47 TLIYPTMRF 55

RESULT 5

H83424

hypothetical protein PA1765 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83424

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83424

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <STO>

A:Cross-references: GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG05154.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1765

Query Match 63.8%; Score 37; DB 2; Length 395;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10

:|::|||::|

Db 292 RQVYPSLLF 301

RESULT 6

D86267

T6J4.4 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001

C:Accession: D86267

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86267

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <STO>
A:Cross-references: GB:AE005172; NID:g9958068; PIDN:AAG09557.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 180;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
|:||||:|
Db 124 RQLVPTKLF 133

RESULT 7

E72342
pmba-related protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72342
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72342

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <ARN>

A:Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0727

C:Superfamily: Escherichia coli pmbA protein

Query Match 60.3%; Score 35; DB 2; Length 435;
Best Local Similarity 54.5%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 11
|:|:|:|:|
Db 135 RVNVPVVMYK 145

RESULT 8

AG0890
probable arylsulfate sulfotransferase [imported] - Salmonella enterica subsp. enterica s
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0890
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AG0890
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-598 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07717.1; PID:g16504269; GSPDB:GN00176
C:Genetics:
A:Gene: STY3370

Query Match 60.3%; Score 35; DB 2; Length 598;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 11
:|:|:|

Db 590 LVHPTOMFK 598

RESULT 9

B96598
hypothetical protein T5A14.3 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B96598
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96598

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-887 <STO>

A:Cross-references: GB:AE005173; NID:g4204259; PIDN:AAD10640.1; GSPDB:GN00141

C:Genetics:

A:Gene: T5A14.3

A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 887;
Best Local Similarity 70.0%; Pred. No. 1.le+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 11
||| ||:| |
Db 696 TVVNPTLMK 705

RESULT 10

H84758
hypothetical protein Atg34620 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84758

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84758

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303 <STO>

A:Cross-references: GB:AE002093; NID:g3128213; PIDN:AAC26693.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg34620

A:Map position: 2

Query Match 58.6%; Score 34; DB 2; Length 303;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
||:|:| |
Db 120 RTELVPVFMF 129

RESULT 11

AD3513
channel protein virB6 homolog [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C;Accession: AD3513
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, P.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AD3513
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-347 <KUR>
 A;Cross-references: GB:AE008918; PIDN:AAL53271.1; PID:g17984152; GSPDB:GN00191
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BMEI0030
 A;Map position: II

Query Match 58.6%; Score 34; DB 2; Length 347;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
 |:|:|:|:
 Db 257 TVVPMYMYK 266

RESULT 12
 S17955
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium leiognathi
 C;Species: Photobacterium leiognathi
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
 C;Accession: S17955
 R;Lee, C.Y.; Szittner, R.B.; Meighen, E.A.
 Eur. J. Biochem. 201, 161-167, 1991
 A;Title: The lux genes of the luminous bacterial symbiont, *Photobacterium leiognathi*, of *Coli*.
 A;Reference number: S17836; MUID:92007870; PMID:1915359
 A;Accession: S17955
 A;Molecule type: DNA
 A;Residues: 1-373 <LEE>
 A;Cross-references: EMBL:M63594; NID:g150687; PIDN:AAA25620.1; PID:g150692
 C;Genetics:
 A;Gene: luxE
 C;Keywords: acid-thiol ligase
 F:364/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 58.6%; Score 34; DB 2; Length 373;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VYPTMMFK 11
 |:|:|:|:
 Db 78 VFPTSMFK 85

RESULT 13
 S15161
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium phocae
 N;Alternate names: acyl-protein synthetase
 C;Species: Photobacterium phosphoreum
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C;Accession: S15161
 R;Soly, R.R.; Meighen, E.A.
 J. Mol. Biol. 219, 69-77, 1991
 A;Title: Identification of the acyl transfer site of fatty acyl-protein synthetase from *Photobacterium phosphoreum*.
 A;Reference number: S15160; MUID:91218179; PMID:2023262
 A;Accession: S15161
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-373 <JMO>
 C;Genetics:
 A;Gene: luxE
 C;Keywords: acid-thiol ligase
 F:364/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 58.6%; Score 34; DB 2; Length 373;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VYPTMMFK 11
 |:|:|:|:
 Db 78 VFPTSMFK 85

RESULT 14

AD0478
 acetylornithine deacetylase (EC 3.5.1.16) [imported] - *Yersinia pestis* (strain CO92)
 C;Species: *Yersinia pestis*
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
 C;Accession: AD0478
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, N.; Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AD0478
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-389 <KUR>
 A;Cross-references: GB:AL590842; PIDN:CAC93392.1; PID:g15981838; GSPDB:GN00175
 C;Genetics:
 A;Gene: argE
 C;Superfamily: succinyl-diaminopimelate desuccinylase
 C;Keywords: hydrolase

Query Match 58.6%; Score 34; DB 2; Length 389;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 |:|:|:|:
 Db 238 TVPYPTMMF 246

RESULT 15

B41317
 O-antigen ligase complex protein rfaL - *Salmonella typhimurium*
 C;Species: *Salmonella typhimurium*
 C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
 C;Accession: B41317
 R;MacLachlan, P.R.; Kadam, S.K.; Sanderson, K.E.
 J. Bacteriol. 173, 7151-7163, 1991
 A;Title: Cloning, characterization, and DNA sequence of the rfaL region for lipopolysaccharide O-antigen synthesis in *Salmonella typhimurium*.
 A;Reference number: A41317; MUID:92041612; PMID:1657881
 A;Accession: B41317
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-404 <MAC>
 A;Cross-references: GB:M73826; NID:g154328; PIDN:AAA27206.1; PID:g154330
 C;Keywords: transmembrane protein

Query Match 58.6%; Score 34; DB 2; Length 404;
 Best Local Similarity 63.6%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
 |:|:|:|:
 Db 305 RVVDYPTWTFK 315

RESULT 16

AE0973
 O-antigen ligase [imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi* (strain ATCC 14029)
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C;Accession: AE0973
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03281.1; PID:g16504902; GSPDB:GN00176
C;Genetics:
A;Gene: waaL

Query Match 58.6%; Score 34; DB 2; Length 404;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RTVVYPTMMFK 11
| | | | |
Db 305 RVVDYPTWTFK 315
| | | | |

RESULT 17
T50785
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50785
R;Bavan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mexico
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 58/1
A;Note: T30N20_30

Query Match 58.6%; Score 34; DB 2; Length 464;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TVVYPTMMF 10
| | | | |
Db 392 TVYPTIAF 400
| | | | |

RESULT 18
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72329
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ARN>
A;Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35899.1; PID:g498134
A;Experimental source: strain MSB8

C;Genetics:
A;Gene: TM0817

Query Match 58.6%; Score 34; DB 2; Length 674;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RTVVYPTMMF 10
| | | | |
Db 192 QTFVYVPMF 201
| | | | |

RESULT 19
A86424
unknown protein, 35070-37205 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86424
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-711 <STO>
A;Cross-references: GB:AE005172; NID:g10092467; PIDN:AAG12869.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 58.6%; Score 34; DB 2; Length 711;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RTVVYPTMMF 10
| | | | |
Db 461 RRVYPTLRY 470
| | | | |

RESULT 20
T13942
UNC-13-B protein - fruit fly (*Drosophila melanogaster*) (fragment)
C;Species: *Drosophila melanogaster*
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13942
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C. J. Biol. Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic transmission
A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13942
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1724 <XUX>
A;Cross-references: EMBL:Y17922; NID:g3893112; PIDN:CAA76942.1; PID:g3893113
C;Genetics:
A;Cross-references: FlyBase:FBgn0025726
A;Note: UNC-13-B
C;Superfamily: protein kinase C zinc-binding repeat homology
F;602-651/Domain: protein kinase C zinc-binding repeat homology <KN>

Query Match 57.8%; Score 33.5; DB 2; Length 1724;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
Qy 1 RTVVYPTMMF 11
| | | | |

db 1437 KTIVLPMTDKTMMFK 1452

RESULT 21
E69798
conserved hypothetical protein yeth - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E69798
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Bertet
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapida, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, M.; Ogawa, K.; Ogilwa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaite, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A68580; MUID:98044033; PMID:9384377
A:Accession: E69798
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-120 <RUN>
A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12535.1; PID:g2633029
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeth

C:Superfamily: Bacillus probable methylglyoxalase yurT

Query Match 56.9%; Score 33; DB 1; Length 120;
Best Local Similarity 54.5%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
| | | | |
D 53 RLVIYPKAMK 63

RESULT 22
A90710
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A90710
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A90710
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034072.1; PID:g13360107; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs0649

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
| | | | |
D 73 RTLVIYPAKM 81

RESULT 23
E85560

regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85560
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <STO>
A:Cross-references: GB:AE005174; NID:g12513506; PIDN:AAG54945.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: rnk

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
| | | | |
D 73 RTLVIYPAKM 81

RESULT 24
I57917

nucleoside diphosphate kinase regulator - Escherichia coli (strain K-12)
N:Alternate names: rnk protein
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 01-Mar-2002
C:Accession: I57917; H64794
R:Schlicman, D.; Shankar, S.; Chakrabarty, A.M.
Mol. Microbiol. 16, 309-320, 1995
A:Title: The Escherichia coli genes sspA and rnk can functionally replace the Pseudom
A:Reference number: I57917; MUID:96015444; PMID:7565093
A:Accession: I57917
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-136 <RES>
A:Cross-references: GB:L37900; NID:g598117; PIDN:AAC36933.1; PID:g598118
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:Cross-references: GB:AE000166; GB:U00096; NID:g1786819; PIDN:AAC73711.1; PID:g17868
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: rnk

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
| | | | |
D 73 RTLVIYPAKM 81

RESULT 25
S29308

hypothetical protein 3 (phaC2 3' region) - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999

C:Accession: S29308; S28380
R:Timm, A.; Steinbuechel, A.
Eur. J. Biochem. 209, 15-30, 1992
A:Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus
A:Reference number: S29303; MUID:93011120; PMID:1396693
A:Accession: S29308
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <TIM>
A:Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47154.1; PID:g45394

Query Match 56.9%; Score 33; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
 |||||
Db 172 RTVVYQIMM 180

Search completed: July 16, 2003, 14:34:15
Job time : 22 secs

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OM protein : protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 10.3333 Seconds
(without alignments)
44.152 Million cell updates/sec

Title: US-09-923-716c-1
Perfect score: 58
Sequence: 1 RTVVYPTMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	65.5	262	DET2_ARATH	Q38944 arabidopsis
2	34	58.6	373	LUXE_PHOLE	P29334 photobacter
3	34	58.6	404	RFAL_SALTY	P26471 salmonella
4	33	56.9	136	RNK_ECOLI	P40679 escherichia
5	33	56.9	193	RCF1_DICDI	O96390 dictyosteli
6	33	56.9	551	SYE_ARCFU	O29979 archaeoglob
7	33	56.9	594	YKP3_KLULA	P05469 kluyveromyc
8	32	55.2	61	PSBK_ORYSA	P12162 oryza sativ
9	32	55.2	61	PSBK_WHEAT	P58273 triticum ae
10	32	55.2	143	B701_HSV6G	P30024 human herpe
11	32	55.2	169	COAD_CHRVI	P71154 chromatium
12	32	55.2	200	CAKB_COTJA	Q98855 coturnix co
13	32	55.2	201	IP23_LYCES	Q43502 lycopersico
14	32	55.2	214	Y473_TREPA	O83486 treponema p
15	32	55.2	421	GLTT_BACCA	P24944 bacillus ca
16	32	55.2	468	VAS1_BOVIN	P40682 bos taurus
17	32	55.2	595	TRPE_ARATH	P32068 arabidopsis
18	32	55.2	603	NU5M_HYLLA	P30319 lylobates i
19	32	55.2	1416	RPOC_TREPA	O83270 treponema p
20	32	55.2	1716	RPAL_RAT	O54889 rattus norv
21	32	55.2	3175	RPOA_EAV	P19811 equine arte
22	31	53.4	157	SMPL_HUMAN	O95807 homo sapien
23	31	53.4	207	YQJL_ECOLI	O46872 escherichia
24	31	53.4	320	DNC_HUMAN	Q9hc21 homo saplen
25	31	53.4	362	MSPL_YEAST	P28737 saccharomyc
26	31	53.4	421	GLTT_BACST	P24943 bacillus st
27	31	53.4	437	SECY_BUCAI	P57571 buchnera ap
28	31	53.4	439	RHGI_HUMAN	Q07960 homo sapien
29	31	53.4	440	AK_CHLPN	O9z610 chlamydia p
30	31	53.4	442	SECY_SYN3	P77964 synechocyst
31	31	53.4	507	PDL_DATGL	O9xf61 datisca glo
32	31	53.4	527	KITH_HSVSA	P12293 herpesvirus
33	31	53.4	601	NU5M_DASNO	O21335 dasyypus nov

34	31	53.4	604	1	NU5M_HORSE	P48656 equus cabal
35	31	53.4	606	1	NU5M_BOVIN	P03920 bos taurus
36	31	53.4	606	1	NU5M_CERSI	O03205 ceratotheri
37	31	53.4	606	1	NU5M_EQUAS	P32485 equus asinu
38	31	53.4	606	1	NU5M_SHEEP	O78756 ovis aries
39	31	53.4	640	1	GIDA_ANASP	Q9yr87 anabaena sp
40	31	53.4	657	1	UVRB_CAMJE	Q9ppm7 campylobact
41	31	53.4	714	1	PBPF_BACSU	P38050 bacillus su
42	31	53.4	1067	1	EG52_XENLA	P1783 xenopus lae
43	31	53.4	1358	1	PGCV_MOUSE	Q62059 mus musculu
44	31	53.4	4196	1	DFHC_SCHPO	O3290 schizosacch
45	30.5	52.6	1968	1	RRPO_PVMR	P17965 potato viru
46	30	51.7	61	1	PSBK_HORVU	P25877 hordeum vul
47	30	51.7	116	1	LUXE_PHOLU	P19842 photorhabdu
48	30	51.7	122	1	XJ41_YEAST	P47121 saccharomyc
49	30	51.7	149	1	YQBN_BACSU	P45930 bacillus su
50	30	51.7	158	1	IP2X_SOLITU	Q00782 solanum tub
51	30	51.7	193	1	RCF2_DICDI	Q9ggs3 dictyosteli
52	30	51.7	221	1	KCY1_BORBU	O51154 borrelia bu
53	30	51.7	238	1	YG26_HAETN	P44278 haemophilus
54	30	51.7	265	1	UL07_HSVSA	Q01028 herpesvirus
55	30	51.7	315	1	VC04_VACCV	P17370 vaccinia vi
56	30	51.7	316	1	VC04_VACCC	P21038 vaccinia vi
57	30	51.7	316	1	VC04_VAVR	P34012 variola vir
58	30	51.7	352	1	GLN1_DAUCA	O22504 daucus caro
59	30	51.7	356	1	GLN1_MEDSA	P04078 medicago sa
60	30	51.7	356	1	GLN1_PHAVU	P04770 phaseolus v
61	30	51.7	356	1	GLNA_VIGAC	P32289 vigna aconl
62	30	51.7	358	1	GLNA_LACSA	P37112 lactuca sat
63	30	51.7	376	1	YG3W_YEAST	P53293 saccharomyc
64	30	51.7	378	1	LUXE_VIBHA	P14286 vibrio harv
65	30	51.7	416	1	PXN1_XENLA	P49263 xenopus lae
66	30	51.7	420	1	PUR2_LISIN	Q92ap4 listeria in
67	30	51.7	426	1	PUR2_LISMO	Q8y6c6 listeria mo
68	30	51.7	426	1	STE2_SACKL	P12384 saccharomyc
69	30	51.7	477	1	LYII_HUMAN	Q14108 homo sapien
70	30	51.7	477	1	LYII_RAT	P27615 rattus norv
71	30	51.7	497	1	YJ92_YEAST	P47158 saccharomyc
72	30	51.7	497	1	SNX2_HUMAN	O60749 homo sapien
73	30	51.7	519	1	SNX2_MOUSE	Q9cwk8 mus musculu
74	30	51.7	521	1	PXL1_SACPS	P79001 saccharomyc
75	30	51.7	536	1	CCAM_DROME	Q9ve00 drosophila

ALIGNMENTS

RESULT 1				
DET2_ARATH				
ID	DET2_ARATH	STANDARD:	PRT:	262 AA.
AC	Q38944: Q9SH83:			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Probable steroid reductase DET2 (EC 1.3.99.-).			
GN	DET2 OR AT2G38050 OR T8P21.4.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=96185496; PubMed=8602526;			
RA	Li J., Nagpal P., Vitart V., McMorris T.C., Chory J.;			
RT	"A role for brassinosteroids in light-dependent development of Arabidopsis."			
RL	Science 272:398-401(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20083487; PubMed=10617197;			

```

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PCEC).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably involved in a reduction step in the
CC biosynthesis of the plant steroid, brassinolide. Defects in DET2
CC leads to defects in light-regulated development.
CC -1- PATHWAY: Brassinolide biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE STEROID 5-ALPHA REDUCTASE FAMILY.
CC -----
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CC -----
DR EMBL; U53860; AAC49264.1; -
DR EMBL; AC007661; AAD32767.1; -
DR EMBL; AY045926; AAK76600.1; -
DR EMBL; AY079337; AAL85068.1; -
DR InterPro: IPR001104; Strd5A_dhc.
DR Pfam: PF02544; Steroid_dh; 1.
DR PROSITE; PS50244; S5A_REDUCTASE; 1.
DR OXidoreductase; Transmembrane.
KW TRANSMEM 13 33
FT TRANSMEM 51 71 POTENTIAL.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT CONFLICT 198 198 C -> R (IN REF. 1).
SQ SEQUENCE 262 AA; 30635 MW; 88291B8A8AF55664 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 262;
Best Local Similarity 45.5%; Pred. No. 1.8;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTWVPTMFK 11
Db 93 RTIIPRLFR 103
II::II::I:

RESULT 2
LUXE_PHOLE STANDARD; PRT; 373 AA.
AC P29334;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase).
GN LUXE.
OS Photobacterium leiognathi.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC Photobacterium.
OX NCBI_TaxID=658;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25521;
RX MEDLINE=92007870; PubMed=1915359;
RA Lee C.Y., Seltner R.B., Meighen E.A.;
RT "The lux genes of the luminous bacterial symbiont, Photobacterium
RT leiognathi, of the ponyfish. Nucleotide sequence, difference in gene
RT organization, and high expression in mutant Escherichia coli.";
RL Eur. J. Biochem. 201:161-167(1991).
CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein -> AMP + diphosphate +
CC an acyl-protein thioester.
CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -----
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CC -----
DR EMBL; M63594; AAA25620.1; -
DR PIR; S17955; S17955.
KW Luminescence; Ligase.
SQ SEQUENCE 373 AA; 43099 MW; 1B31848B00BF9921 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 373;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVPTMMFK 11
Db 78 VFPTSMFK 85
I::I::I::I:

RESULT 3
REAL_SALTY STANDARD; PRT; 404 AA.
AC P26471;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE O-antigen ligase.
GN REAL OR WALR OR REPT OR STM3713.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=92041612; PubMed=1657881;
RA MacLachlan P.R., Kadam S.K., Sanderson K.E.;
RT "Cloning, characterization, and DNA sequence of the rfaLK region for
RT lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
RL J. Bacteriol. 173:7151-7163(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -1- FUNCTION: ADDS THE O-ANTIGEN ON THE GLUCOSE(II) GROUP OF LPS.
CC -1- PATHWAY: Lipopolysaccharide core biosynthesis.

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OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214006; PubMed=10198067;
RA Rivero F., Albrecht R., Dislich H., Bracco E., Graciotti L.,
RA Bozzaro S., Noegel A.A.;
RT "Racfl", a novel member of the Rho protein family in Dictyostelium
RT discoidium, associates transiently with cell contact areas,
RT macropinosomes and phagosomes."
RL Mol. Biol. Cell 10:1205-1219(1999).
CC -!- FUNCTION: MIGHT ACT IN CONCERT AND/OR SHARE FUNCTIONS WITH OTHER
CC MEMBERS OF THE RHO FAMILY IN THE REGULATION OF A SUBSET OF
CC CYTOSKELETAL REARRANGEMENTS THAT ARE REQUIRED FOR THESE PROCESSES.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC -----
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CC -----
DR EMBL; AF037042; AAD09143.1;
DR HSSP; P21181; IAM4.
DR DictyDb; D077777; racfl.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR001230; Prenyl_site.
DR InterPro; IPR001806; Ras_trnsmg.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMG.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT FT 57 61 GTP (BY SIMILARITY).
FT NP_BIND 115 118 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (POTENTIAL).
FT LIPID 190 190 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 193 AA; 21830 MW; 206E814C823E3B2E CRC64;

Query Match 56.9%; Score 33; DB 1; Length 193;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMFK 11
Db 173 RSVIYENKLIK 183
I:|:|:|:|

RESULT 6
SYE_ARCFU STANDARD; PRT; 551 AA.
AC 029979;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GLURS)
DE GN GLTX OR AF0260.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

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RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) -> AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AE001087; AAB90966.1;
DR HSSP; P00962; IGTR.
DR TIGR; AF0260;
DR InterPro; IPR004526; GltX_arch.
DR InterPro; IPR000924; Glu_trna-synt_lc.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00749; tRNA-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00463; gltX_arch; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
FT Complete proteome.
FT SITE 100 110 "HIGH" REGION.
SQ SEQUENCE 551 AA; 64402 MW; A985A300C6B68F2E CRC64;

Query Match 56.9%; Score 33; DB 1; Length 551;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMFK 11
Db 270 VVYPTLDFE 278
I:|:|:|:|

RESULT 7
YKP3_KLULA STANDARD; PRT; 594 AA.
AC P05469;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hypothetical killer plasmid pGKL-2 protein 3.
OS Kluyveromyces lactis (Yeast).
OG plasmid pGKL-2.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
RX MEDLINE=88289339; PubMed=3041369;
RA Tommasino S., Ricci S., Galeotti C.L.;
RT "Genome organization of the killer plasmid pGKL2 from Kluyveromyces
RT lactis."
RL Nucleic Acids Res. 16:5863-5878(1988).
CC -!- FUNCTION: THE PRESENCE OF THE TWO LINEAR PLASMIDS, TERMED
CC PGKL1 AND PGKL2, IN STRAINS OF KLUYVEROMYCES LACTIS CONFERS
CC THE KILLER PHENOTYPE TO THE HOST CELL, BY PROMOTING THE
CC SECRETION OF A TOXIN ABLE TO INHIBIT THE GROWTH OF SENSITIVE

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CC STRAINS.
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CC -----
CC EMBL; X07776; CAA30604.1; -
CC PIR; S00961; S00961.
CC InterPro; IPR000977; DNA_ligase.
CC Pfam; PF01068; DNA_ligase; 1.
CC Hypothetical protein; Plasmid.
CC SEQUENCE 594 AA; 70527 MW; 6AE57D37618BF6B0 CRC64;
CC -----
Query Match 56.9%; Score 33; DB 1; Length 594;
Best Local Similarity 36.4%; Pred. No. 45;
Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
CC -----
Cc 1 RTVYPTMMFK 11
Cc :|||::|:
Cc 80 RSTMPSLIFR 90
Cc -----
RESULT 8
PSBK_ORYSA
ID PSBK_ORYSA STANDARD; PRT; 61 AA.
AC P12162;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II reaction center protein K precursor (PSII-K).
GN PSBK.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=89364598; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugliara M.;
RA "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct trna genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC OF PHOTOSYSTEM II.
CC -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC -----
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CC -----
CC EMBL; X15901; CAA34010.1; -
CC PIR; JQ0203; F2R2KS.
CC InterPro; IPR003687; PSII_PsbK.
CC Pfam; PF02533; PsbK; 1.
CC Photosystem II; Chloroplast.
CC PROPEP 1 24 POTENTIAL.
CC CHAIN 25 61 PHOTOSYSTEM II REACTION CENTER PROTEIN K.
CC SEQUENCE 61 AA; 6982 MW; BBC361067C4158F5 CRC64;
CC -----

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Query Match 55.2%; Score 32; DB 1; Length 61;
Best Local Similarity 55.6%; Pred. No. 6.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Cc 2 TVVYPTMMF 10
Cc :|||:|
Cc 14 SVIYPTSF 22
Cc -----
RESULT 9
PSBK_WHEAT
ID PSBK_WHEAT STANDARD; PRT; 61 AA.
AC P58273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Photosystem II reaction center protein K precursor (PSII-K).
GN PSBK.
OS Triticum aestivum (Wheat).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA Gojobori T., Murai R., Murai K., Matsuo Y., Ohmishi Y., Tajiri H.,
RA Tsunewaki K.;
RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT complete sequence and contig clones.";
RL Plant Mol. Biol. Rep. 18:243-253(2000).
CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC OF PHOTOSYSTEM II.
CC -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC -----
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CC -----
CC EMBL; AB042240; BAB47017.1; -
CC InterPro; IPR003687; PSII_PsbK.
CC Pfam; PF02533; PsbK; 1.
CC Photosystem II; Chloroplast.
CC PROPEP 1 24 BY SIMILARITY.
CC CHAIN 25 61 PHOTOSYSTEM II REACTION CENTER PROTEIN K.
CC SEQUENCE 61 AA; 7030 MW; 467901067C4158FD CRC64;
Cc -----
Query Match 55.2%; Score 32; DB 1; Length 61;
Best Local Similarity 55.6%; Pred. No. 6.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Cc 2 TVVYPTMMF 10
Cc :|||:|
Cc 14 SVIYPTSF 22
Cc -----
RESULT 10
B701_HSV6G
ID B701_HSV6G STANDARD; PRT; 143 AA.
AC P30024;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein B701.
OS Human herpesvirus (type 6 / strain GS) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92148942; PubMed=1310766;
RA Geng Y., Chandran B., Josephs S.F., Wood C.;
RT "Identification and characterization of a human herpesvirus 6 gene 1
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter.";
RL J. Virol. 66:1564-1570(1992).
CC -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
CC SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
CC DIRECTLY OR INDIRECTLY.
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CC -----
DR EMBL: M81789; ; NOT_ANNOTATED_CDS.
DR PIR: A42186; WMBE6H.
KW Transcription regulation; Trans-acting factor; Activator.
SQ SEQUENCE 143 AA; 16385 MW; D0CB4D7C2422AAD8 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 143;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFM 10
Db 50 KTLLEPKTMF 59
:l:::lll

RESULT 11
COAD_CHRVI
ID COAD_CHRVI STANDARD; PRT; 169 AA.
AC P71154;
AT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
DE phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
DE pyrophosphorylase).
GN COAD OR KDTB.
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
OC Allochromatium.
OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / ATCC 17899 / DSM 180;
RX MEDLINE=96328257; PubMed=8765743;
RA Moulis J.M.;
RT "Molecular cloning and expression of the gene encoding Chromatium
RT vinosum 2[4Fe-4S] ferredoxin.";
RL Biochim. Biophys. Acta 1308:12-14(1996).
CC -!- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
CC PHOSPHOPANTHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
CC PYROPHOSPHATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
CC dephospho-CoA.
CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE COAD FAMILY.
CC -----
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CC -----
DR EMBL: U45327; AAC44332.1; -
DR DR HSSP; P23875; 1B6T.
DR InterPro: IPR004821; Cyt_tran_rel.
DR InterPro: IPR004820; Cytidylyltransf.
DR InterPro: IPR001980; LPS_biosynth.
DR Pfam: PF01467; Cytidylyltransf; 1.
DR PRINTS: PR01020; LPSBIOSNTHSS.
DR TIGRFAMs: TIGR00125; cyt_tran_rel; 1.
KW Transferase; Nucleotidylyltransferase; Coenzyme A biosynthesis.
SQ SEQUENCE 169 AA; 18559 MW; 5126FD2BF32824AC CRC64;

Query Match 55.2%; Score 32; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYP 6
Db 2 RTVVYP 7
:llllll

RESULT 12
CAKB_COTJA
ID CAKB_COTJA STANDARD; PRT; 200 AA.
AC Q98855;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative calcium-activated potassium channel beta subunit.
GN CO6.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224079; PubMed=9070660;
RA Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT "Suppression in transformed avian fibroblasts of a gene (CO6)
RT encoding a membrane protein related to mammalian potassium channel
RT regulatory subunits."
RL Oncogene 14:1109-1116(1997).
CC -!- FUNCTION: POTASSIUM CHANNEL PROTEIN WHICH MAY MODULATE THE
CC PROPERTIES OF THE PORE-FORMING ALPHA SUBUNIT (BY SIMILARITY).
CC -!- SUBUNIT: THE CALCIUM-ACTIVATED POTASSIUM CHANNEL IS COMPOSED OF
CC AT LEAST TWO SUBUNITS: A PORE-FORMING ALPHA SUBUNIT AND A
CC REGULATORY BETA SUBUNIT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC -----
DR EMBL: U67865; AAC26967.1; -
DR InterPro: IPR003930; BK_channel_beta.
DR Pfam: PF03185; Cakb; 1.
KW Ionic channel; Transmembrane; Glycoprotein.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 200 AA; 22677 MW; B7A612D8973F711F CRC64;

Query Match 55.2%; Score 32; DB 1; Length 200;

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Best Local Similarity 55.6%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TVVYPTMMF 10
Db 169 TFLWPTLMF 177

RESULT 13
IP23_LYCES
ID IP23_LYCES STANDARD; PRT; 201 AA.
AC Q43502;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteinase inhibitor type II CEVI57 precursor.
GN CEVI57.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rutgers; TISSUE=Leaf;
RX MEDLINE=96252900; PubMed=8672818;
RA Gadea J., Mayda E., Conejero V., Vera P.;
RT "Characterization of defense-related genes ectopically expressed in
RT viroid-infected tomato plants";
RL Mol. Plant Microbe Interact. 9:409-415(1996).
CC -1- INDUCTION: BY VIROID INFECTION.
CC -1- SIMILARITY: BELONGS TO THE POTATO TYPE II PROTEINASE INHIBITOR
CC FAMILY.
CC -----
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CC -----
CC EMBL; X94946; CAA64416.1; -.
CC HSSP; P01080; 45GB.
CC InterPro; IPR003465; Prot_inhib.
CC Pfam; PF02428; Prot_inhib_II; 3.
CC Serine protease inhibitor; Repeat; Signal.
KW SIGNAL 1 23
FT CHAIN 24 201 PROTEINASE INHIBITOR TYPE II CEVI57.
FT REPEAT 27 83 1.
FT REPEAT 84 143 2.
FT REPEAT 144 199 3.
FT ACT_SITE 32 33 INTERACTION WITH TRYPSIN (PROBABLE).
FT ACT_SITE 147 148 INTERACTION WITH TRYPSIN (PROBABLE).
SQ SEQUENCE 201 AA; 21419 MW; A3FCAB9377308590 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 201;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTVYPT 7
Db 106 KTIIVPT 112

RESULT 14
Y473_TREPA
ID Y473_TREPA STANDARD; PRT; 214 AA.
AC O83486;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0473.

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GN TP0473.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RT Science 281:375-388(1998).
RL Science 281:375-388(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
CC EMBL; AE001224; AAC65467.1; -.
CC TIGR; TP0473; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 4 23 POTENTIAL.
FT TRANSMEM 35 57 POTENTIAL.
FT TRANSMEM 67 89 POTENTIAL.
FT TRANSMEM 96 118 POTENTIAL.
FT TRANSMEM 128 150 POTENTIAL.
FT TRANSMEM 155 177 POTENTIAL.
FT TRANSMEM 187 209 POTENTIAL.
SQ SEQUENCE 214 AA; 24001 MW; 1497AA7E15DFAE92 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 214;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RTVYPTMM 9
Db 186 RTVYPTSM 194

RESULT 15
GLTT_BACCA
ID GLTT_BACCA STANDARD; PRT; 421 AA.
AC P24944;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier
DE protein).
GN GLTT.
OS Bacillus caldotenax.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1395;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93062018; PubMed=1359385;
RA Tolner B., Poolman B., Konings W.N.;
RT "Characterization and functional expression in Escherichia coli of
RT the sodium/proton/glutamate symport proteins of Bacillus
RT steatothermophilus and Bacillus caldotenax.";
RL Mol. Microbiol. 6:2845-2856(1992).
CC -1- FUNCTION: THIS CARRIER PROTEIN IS PART OF THE NA(+)-DEPENDENT,
CC BINDING-PROTEIN-INDEPENDENT GLUTAMATE-ASPARTATE TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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CC CC -1- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
CC CC (SDF, TC 2.A.23).
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: M86509; AAA22493.1; -
CC CC PIR: S26246; S26246.
CC CC InterPro: IPR001991; Na/dico_symp.
CC CC Pfam: PF00375; SDF; 1.
CC CC PROSITE: PS00713; NA_DICARBOXYL_SYMPT_1; 1.
CC CC PROSITE: PS00714; NA_DICARBOXYL_SYMPT_2; 1.
CC CC Transport; Transmembrane; Symport.
CC CC -----
CC CC DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
CC CC TRANSSEM 4 24 POTENTIAL.
CC CC DOMAIN 25 43 EXTRACELLULAR (POTENTIAL).
CC CC TRANSSEM 44 64 POTENTIAL.
CC CC DOMAIN 65 77 CYTOPLASMIC (POTENTIAL).
CC CC TRANSSEM 78 98 POTENTIAL.
CC CC DOMAIN 99 148 EXTRACELLULAR (POTENTIAL).
CC CC TRANSSEM 149 169 POTENTIAL.
CC CC DOMAIN 170 198 CYTOPLASMIC (POTENTIAL).
CC CC TRANSSEM 199 219 POTENTIAL.
CC CC DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).
CC CC TRANSSEM 223 243 POTENTIAL.
CC CC DOMAIN 244 244 CYTOPLASMIC (POTENTIAL).
CC CC TRANSSEM 245 265 POTENTIAL.
CC CC DOMAIN 266 306 EXTRACELLULAR (POTENTIAL).
CC CC TRANSSEM 307 327 POTENTIAL.
CC CC DOMAIN 328 330 CYTOPLASMIC (POTENTIAL).
CC CC TRANSSEM 331 351 POTENTIAL.
CC CC DOMAIN 352 372 POTENTIAL.
CC CC TRANSSEM 373 421 CYTOPLASMIC (POTENTIAL).
CC CC SEQUENCE 421 AA; 45345 MW; 10ABBE12EDD1E7E4 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 421;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VYVPTMMF 10
DB 226 VYVATMLF 233
|||||

RESULT 16
VASI_BOVIN
ID VASI_BOVIN STANDARD; PRT; 468 AA.
AC P40682;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14) (V-ATPase S1
DE subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit).
GN ATP6IP1 OR ATP6S1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OC NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 378-388.
RC TISSUE-Adrenal chromaffin;
RX MEDLINE=95014142; PubMed=7929063;
RA Supek F., Supekova L., Mandiyan S., Pan Y.-C.E., Nelson H., Nelson N.;
RT "A novel accessory subunit for vacuolar H(+)-ATPase from chromaffin
RT granules."
RL J. Biol. Chem. 269:24102-24106(1994).
CC -1- FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY

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CC CC OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC CC H(+)(Out).
CC CC -1- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC CC -----
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CC CC -----
CC CC EMBL: U10039; AAA50752.1; -
CC CC ATP synthetase; Hydrogen ion transport; Hydrolase; ATP-binding;
CC CC Transmembrane; Glycoprotein; Signal.
CC CC SIGNAL 1 35 POTENTIAL.
CC CC CHAIN 36 468 VACUOLAR ATP SYNTHASE SUBUNIT S1.
CC CC TRANSSEM 418 438 POTENTIAL.
CC CC CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC SEQUENCE 468 AA; 51781 MW; BF2C42D56ABB1B6D CRC64;

Query Match 55.2%; Score 32; DB 1; Length 468;
Best Local Similarity 87.5%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVVVPTM 8
DB 244 RTVVVPTM 251
|||||

RESULT 17
TRPE_ARATH
ID TRPE_ARATH STANDARD; PRT; 595 AA.
AC P32068;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Anthranilate synthase component I-1, chloroplast precursor
DE (EC 4.1.3.27).
GN ASA1 OR AT5G05730 OR MJJ3.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=93005721; PubMed=1392592;
RX Niyyogi K.K., Fink G.R.;
RA "Two anthranilate synthase genes in Arabidopsis: defense-related
RA regulation of the tryptophan pathway."
RL Plant Cell 4:721-733(1992).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones."
RL DNA Res. 4:215-230(1997).
CC -1- CATALYTIC ACTIVITY: Chorismate + L-glutamine -> anthranilate +
CC pyruvate + L-glutamate.

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CC -!- PATHWAY: Tryptophan biosynthesis; first step.
CC -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.
CC -!- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -----
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CC -----
DR EMBL; M92353; AAA32738.1; -.
DR EMBL; AB005237; BAB09667.1; -.
DR PIR; S27751; S27751.
DR HSSP; Q06128; 1QDL.
DR InterPro; IPR005256; Anth_synthI.
DR InterPro; IPR000350; Chorismate_bind.
DR Pfam; PF00425; chorismate_bind; 1.
DR PRINTS; PR00095; ANTSNTHASEI.
DR PRODOM; PD00079; Chorismate_bind; 1.
DR TIGRFAMs; TIGR00564; trpe_most; 1.
KW Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide;
KW Multigene family.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 595 ANTHRANILATE SYNTHASE COMPONENT I-1.
SQ SEQUENCE 595 AA; 66311 MW; 674175416A2726F0 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 595;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVYPT 7
Db 526 RTVEPT 532
|||||

RESULT 18
ID NUSM_HYLLA STANDARD; PRT; 603 AA.
AC P03919;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN MTND5 OR ND5 OR NADH5.
OS Hylobates lar (Common gibbon).
OC Mitochondrion.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
CC NCBI_TaxID=9580;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-Ester.
RA Arnason U., Gullberg A., Xu X.;
RT "A complete mitochondrial DNA molecule of the white-handed gibbon,
RT Hylobates lar, and comparison among individual mitochondrial genes of
RT all hominoid genera."
RL Hereditas 124:185-189(1996).
RN [2]
RP SEQUENCE OF 1-79 FROM N.A.
RX MEDLINE=82242101; PubMed=6284948;
RA Brown W.M., Prager E.M., Wang A., Willson A.C.;
RT "Mitochondrial DNA sequences of primates: tempo and mode of
RT evolution."
RL J. Mol. Evol. 18:225-239(1982).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----

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CC -----
DR EMBL; X99256; CAA67638.1; -.
DR EMBL; V00659; CAA24025.1; -.
DR PIR; A00449; A00449.
DR InterPro; IPR003916; NADhub_oxred5.
DR InterPro; IPR001750; Oxidored_q1.
DR InterPro; IPR001516; Oxidored_q1_N.
DR Pfam; PF00361; oxidored_q1; 1.
DR Pfam; PF00662; oxidored_q1_N; 1.
DR PRINTS; PR01434; NADHDHGNASE5.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 603 AA; 67360 MW; 3BFF99C6EA7BCE70 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 603;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VYPTMMF 10
Db 48 LFTPTMF 54
|||||

RESULT 19
ID RPOC_TREPA STANDARD; PRT; 1416 AA.
AC O83270;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR TP0242.
OS Treponema pallidum.
CC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
CC NCBI_TaxID=160;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC [RNA](N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----

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CC EMBL; AE001205; AAC65230.1; -
DR HSP; Q9KWU6; IHOM.
DR TIGR; TP0242; -
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 2.
KW Transferase; DNA-directed RNA polymerase; Transcription;
KW Complete proteome.
SQ SEQUENCE 1416 AA; 159789 MW; 78D0EB6A1CA7C9C CRC64;

Query Match 55.28; Score 32; DB 1; Length 1416;
Best Local Similarity 71.48; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVYPT 7 PRT; 1716 AA.
DB 486 RTVYPS 492
II:III:
- - - - -
RESULT 20
ID RPA1_RAT STANDARD; PRT; 1716 AA.
AC Q54889;
DT 15-DEC-1998 (Rel. 37, Created)
DT 13-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA
DE polymerase I 194 kDa subunit) (RPA194).
GN POLR1A OR RPA1-4 OR RPA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086309; PubMed=9422795;
RA Hannan R.D., Hempel W.M., Cavanaugh A., Arino T., Dimitrov S.I.,
RA Moss T., Rothblum L.;
RT "Affinity purification of mammalian RNA polymerase I. Identification
of an associated kinase.";
RL J. Biol. Chem. 273:1257-1267(1998).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
CC RIBOSOMAL DNA UNITS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate +
CC {RNA}(N).
CC -!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
CC DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS THE LARGEST COMPONENT OF
CC RNA POLYMERASE I.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND 5.8S GENES.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC
CC EMBL; AF025425; BAB94601.1; -
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 2.
KW Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
-

KW Zinc-finger; Nuclear protein.
FT ZN_FING 64 80 C2H2-TYPE (POTENTIAL).
SQ SEQUENCE 1716 AA; 194191 MW; E8EE15BC23E60941 CRC64;

Query Match 55.28; Score 32; DB 1; Length 1716;
Best Local Similarity 50.08; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
DB 224 TITYPAVHK 233
II:III:
- - - - -
RESULT 21
RPOA_EAV
ID RPOA_EAV STANDARD; PRT; 3175 AA.
AC P19811; Q88625;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE POL polyprotein (ORF1A/1B) [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
GN POL.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bucyrus;
RX MEDLINE=91237805; PubMed=1851863;
RA den Boon J.A., Snijder E.J., Chirnside E.D., de Vries A.A.F.,
RA Horzinek M.C., Spaan W.J.M.;
RT "Equine arteritis virus is not a togavirus but belongs to the
RT coronaviruslike superfamily.";
RL J. Virol. 65:2910-2920(1991).
RN [2]
RP SEQUENCE OF 1-17 FROM N.A.
RC STRAIN=Bucyrus;
RX MEDLINE=90287699; PubMed=2162519;
RA de Vries A.A.F.; Chirnside E.D., Bredenoek P.J., Gravestien L.A.,
RA Horzinek M.C., Spaan W.J.M.;
RT "All subgenomic mRNAs of equine arteritis virus contain a common
RT leader sequence.";
RL Nucleic Acids Res. 18:3241-3247(1990).
CC -!- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC ROLE FOR NTP-BINDING PROTEINS IN RNA DUPLEX UNWINDING HAS BEEN
CC SUGGESTED. ALSO CONTAINS A PROTEASE DOMAIN.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate + N diphosphate +
CC {RNA}(N).
CC -!- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC FOR 1727-ASN AND 1728-LEU.
CC -!- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC OF TOROVIRUSES.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S32.
CC
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CC
CC EMBL; X53459; CAA37539.1; ALT_SEQ.
DR EMBL; X53459; CAA37540.1; ALT_SEQ.
DR EMBL; X52277; CAA36520.1; -
DR PIR; S10158; S10158.
DR PIR; A39925; RRWVEV.
DR MEROPS; C31.UNW; -
DR MEROPS; C32.001; -
DR MEROPS; C33.001; -
DR MEROPS; C33.001; -
DR MEROPS; S32.001; -

```
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1; 1.
KW RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW Hydrolase; Serine protease; Zinc-finger.
FT CHAIN 1 1727 ORF1A.
FT CHAIN 1728 3175
FT DOMAIN 1080 1220 TRYPSIN-LIKE SERINE PROTEASE.
FT DOMAIN 1218 1506 HELICASE.
FT DOMAIN 2098 2306 POLYMERASE.
FT ACT_SITE 1103 1103 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1129 1129 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1184 1184 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ZN_FING 2368 2414 BY SIMILARITY.
FT NP_BIND 2528 2535 ATP (BY SIMILARITY).
SQ SEQUENCE 3175 AA; 345275 MW; ED5C8BA0E31DE695 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 3175;
Best Local Similarity 83.3%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 5 YPTMFM 10
DB 1369 YPTMFM 1374

RESULT 22
SMPL_HUMAN STANDARD; PRT; 157 AA.
AC O95807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small membrane protein 1.
GN SMPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu G.;
RT "A new member of the 18 kDa small membrane protein family in human.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain.
RC MEDLINE=21154917; PubMed=11230166;
RX Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansgorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
[3]
RN [3]
RP SEQUENCE FROM N.A. AND VARIANT VAL-58.
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO C21ORF4.
-----
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DR EMBL; AF081282; AAD17754.1; -.
DR EMBL; AL136627; CAB66562.1; -.
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DR EMBL; AF458851; AAL51108.1; -.
DR MIN; 605348; -.
KW Transmembrane; Polymorphism.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 95 115 POTENTIAL.
FT TRANSMEM 126 146 POTENTIAL.
FT VARIANT 58 58 A -> V.
FT VARIANT 141 141 /FTid=VAR_013121.
FT VARIANT 141 141 F -> L.
FT VARIANT 141 141 /FTid=VAR_007851.
SQ SEQUENCE 157 AA; 17400 MW; 8CDF89AA23EBB1FA CRC64;

Query Match 53.4%; Score 31; DB 1; Length 157;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VVYPTM 8
DB 44 VVYPTM 49

RESULT 23
YQJL_ECOLI STANDARD; PRT; 207 AA.
ID YQJL_ECOLI
AC Q46872;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yqj1.
GN YQJ1 OR B3071.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655; PubMed=9278503;
RC MEDLINE=97426617;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Glesner C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
-----
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-----
DR EMBL; U28379; AAA89150.1; -.
DR EMBL; AE000389; AAC76106.1; -.
DR EcoGene: EG12954; YQJ1.
DR InterPro: IPR005149; PadR.
DR Pfam: PF03551; PadR; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 23401 MW; DD3D108D83E087F7 CRC64;

Query Match 53.4%; Score 31; DB 1; Length 207;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMFM 10
DB 99 VVYPTMFM 106

RESULT 24
DNC_HUMAN
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ID AC DNC HUMAN STANDARD; PRT; 320 AA.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling protein 1).
GN SLC25A19 OR DNC OR MUP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX PubMed=11226231;
RA Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.;
RT "The human mitochondrial deoxynucleotide carrier and its role in the toxicity of nucleoside antivirals";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Renard S., Mondesert G., Besnard F.;
RT "MUP 1, a mitochondrial uncoupling protein.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Responsible for the uptake of deoxynucleotides into the matrix of the mitochondria. Transports all four deoxy NDPs, and, less efficiently, the corresponding dNTPs. Does not transport dNTPs, NTPs, deoxynucleosides, nucleosides, purines, or pyrimidines. Supply deoxynucleotides to the mitochondrial matrix for conversion to triphosphates and incorporation into mitochondrial DNA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined except for placenta. Highest levels in colon, kidney, lung, testis, spleen, and brain.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- DISEASE: Likely to be medically important by providing the means of uptake into mitochondria of nucleoside analogs, leading to the mitochondrial impairment that underlies the toxic side effects of such drugs in the treatment of viral illnesses, including AIDS, and in cancer therapy.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC
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CC
CC EMBL; AJ251857; CAC27560.1; -
DR EMBL; AJ301616; CAC37793.1; -
DR EMBL; AF182404; AAG16903.1; -
DR EMBL; BC001075; AAH01075.1; -
DR EMBL; BC005120; AAH05120.1; -
DR Genew; HGNC:14409; SLC25A19.
DR MIM; 606521; -
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_cart; 3
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
KW TRANSMEM 19 39 POTENTIAL.
FT TRANSMEM 87 107

FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 293 313 POTENTIAL.
SQ SEQUENCE 320 AA; 35511 MW; 57CE0F01D538B1BE CRC64;
Query Match 53.4%; Score 31; DB 1; Length 320;
Best local Similarity 45.5%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 RTVVYPTMMFK 11
Db 231 KTLTYPLDLFK 241
:1: 11 :11
:1: 11 :11

RESULT 25

MSPI_YEAST STANDARD; PRT; 362 AA.
ID MSPI_YEAST
AC P28737;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MSPI protein (TAT-binding homolog 4).
GN MSPI OR YTA4 OR YGR028W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF747-19D;
RX MEDLINE=94043260; PubMed=8226973;
RA Nakai M., Endo T., Hase T., Matsubara H.;
RT "Intramitochondrial protein sorting. Isolation and characterization of the yeast Mspl gene which belongs to a novel family of putative ATPases";
RL J. Biol. Chem. 268:24262-24269(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=95274317; PubMed=7754704;
RA Schnell R., Mannhaupt G., Stucka R., Tauer R., Ehmlé S., Schwarzlöse C., Vetter I., Feldmann H.;
RT "Identification of a set of yeast genes coding for a novel family of putative ATPases with high similarity to constituents of the 26S protease complex";
RL Yeast 10:1141-1155(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=97435481; PubMed=9290212;
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII";
RL Yeast 13:1077-1090(1997).
RN [4]
RP SEQUENCE OF 280-362 FROM N.A.
RC STRAIN=SC167;
RX MEDLINE=92204135; PubMed=1552903;
RA Lisowsky T.;
RT "Dual function of a new nuclear gene for oxidative phosphorylation and vegetative growth in yeast";
RL Mol. Gen. Genet. 232:58-64(1992).
CC -1- FUNCTION: INVOLVED IN INTRAMITOCHONDRIAL SORTING OF PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial outer membrane.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC
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CC -----
DR EMBL; X68055; CAA48191.1; -.
DR EMBL; X81069; CAA56956.1; -.
DR EMBL; Z72813; CAA97015.1; -.
DR EMBL; X60722; -. NOT_ANNOTATED_CDS.
DR PIR; S20468; S20468.
DR PIR; S37410; S37410.
DR SGD; S0003260; MSP1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_sub.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW ATE-binding; Mitochondrion; Outer membrane; Transmembrane.
FT DOMAIN 1 12 INTERMEMBRANE (POTENTIAL).
FT TRANSMEM 13 28 POTENTIAL.
FT DOMAIN 29 362 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 133 140 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 40343 MW; 1B3562A32F47F434 CRC64;

Query Match 53.4%; Score 31; DB 1; Length 362;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMM 9
Db 106 SVIYPLMM 113

```

Search completed: July 16, 2003, 14:34:57
Job time : 16.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:45 ; Search time 41.6667 seconds
(without alignments)
54.396 Million cell updates/sec

Title: US-09-923-716c-1

Perfect score: 58

Sequence: 1 RTVVPTMWER 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

SPTRMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	333	16 Q55184	Q55184 synechocyst
2	41	70.7	974	5 O01574	O01574 caenorhabdi
3	38	65.5	394	16 Q9CIU3	Q9CIU3 lactococcus
4	37	63.8	390	10 Q8VWX1	Q8VWX1 perilla fru
5	37	63.8	391	10 Q9ZPP7	Q9ZPP7 perilla fru
6	37	63.8	395	16 Q912X4	Q912X4 pseudomonas
7	36	62.1	512	10 Q8LUC5	Q8LUC5 arabidopsis
8	35	60.3	180	10 Q9FX69	Q9FX69 arabidopsis
9	35	60.3	254	10 Q93ZC5	Q93ZC5 arabidopsis
10	35	60.3	258	10 Q9LS01	Q9LS01 arabidopsis
11	35	60.3	264	16 Q8ZLZ1	Q8ZLZ1 salmonella
12	35	60.3	282	10 Q94JV3	Q94JV3 arabidopsis
13	35	60.3	320	11 Q8VGS2	Q8VGS2 mus musculu
14	35	60.3	435	16 Q9WZ16	Q9WZ16 thermotoga
15	35	60.3	504	12 Q9EME6	Q9EME6 amsacta moo
16	35	60.3	598	16 Q8Z3N6	Q8Z3N6 salmonella

RESULT 1

Q55184 PRELIMINARY: PRT; 333 AA.
ID Q55184
AC Q55184;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein sll0456.
GN Sll0456.

ALIGNMENTS

17	35	60.3	705	5 Q8SWA5	Q8SWA5 encephalito
18	35	60.3	733	10 Q8S7E2	Q8S7E2 oryza sativ
19	35	60.3	735	10 Q9FJR9	Q9FJR9 arabidopsis
20	35	60.3	887	10 Q9ZVY2	Q9ZVY2 arabidopsis
21	35	60.3	1030	3 Q9HFQ9	Q9HFQ9 emericeella
22	34	58.6	54	12 Q84121	Q84121 influenzavi
23	34	58.6	173	13 Q8U0Z6	Q8U0Z6 brachydanio
24	34	58.6	180	16 Q981D0	Q981D0 rhizobium l
25	34	58.6	212	16 Q8XNC4	Q8XNC4 clostridium
26	34	58.6	217	17 Q9HUH4	Q9HUH4 halobacteri
27	34	58.6	303	10 Q64685	Q64685 arabidopsis
28	34	58.6	316	10 Q9LSV4	Q9LSV4 arabidopsis
29	34	58.6	320	17 Q8U223	Q8U223 pyrococcus
30	34	58.6	322	4 Q96LB2	Q96LB2 homo sapien
31	34	58.6	322	4 Q8TDD9	Q8TDD9 homo sapien
32	34	58.6	322	4 Q8TDD8	Q8TDD8 homo sapien
33	34	58.6	347	2 Q9KIS7	Q9KIS7 brucella ab
34	34	58.6	347	16 Q8YDZ2	Q8YDZ2 brucella me
35	34	58.6	373	2 P95523	P95523 photobacter
36	34	58.6	373	2 Q52100	Q52100 photobacter
37	34	58.6	389	16 Q8ZA85	Q8ZA85 versinia pe
38	34	58.6	404	16 Q8Z2F8	Q8Z2F8 salmonella
39	34	58.6	464	10 Q9LEW3	Q9LEW3 arabidopsis
40	34	58.6	530	17 Q973Z9	Q973Z9 sulfolobus
41	34	58.6	674	16 Q9WZS4	Q9WZS4 thermotoga
42	34	58.6	711	10 Q9C8R8	Q9C8R8 arabidopsis
43	33.5	57.8	1304	5 Q96959	Q96959 drosophila
44	33.5	57.8	1508	5 Q8T049	Q8T049 drosophila
45	33.5	57.8	1724	5 Q96960	Q96960 drosophila
46	33.5	57.8	1752	5 Q9U4K9	Q9U4K9 drosophila
47	33.5	57.8	1810	5 Q9V483	Q9V483 drosophila
48	33	56.9	120	16 Q31535	Q31535 bacillus su
49	33	56.9	159	8 Q950X8	Q950X8 tetrahymena
50	33	56.9	205	2 Q51516	Q51516 pseudomonas
51	33	56.9	205	16 Q9HOC4	Q9HOC4 pseudomonas
52	33	56.9	221	16 Q8ZDB7	Q8ZDB7 yersinia pe
53	33	56.9	237	10 Q8RX02	Q8RX02 arabidopsis
54	33	56.9	261	10 Q9SUW6	Q9SUW6 arabidopsis
55	33	56.9	299	4 Q9NXA8	Q9NXA8 homo sapien
56	33	56.9	310	4 Q9Y6E6	Q9Y6E6 homo sapien
57	33	56.9	390	16 Q8YFX4	Q8YFX4 brucella me
58	33	56.9	457	17 Q9HLH0	Q9HLH0 thermoplasma
59	33	56.9	457	17 Q978Q5	Q978Q5 thermoplasma
60	33	56.9	474	10 Q43541	Q43541 lilium long
61	33	56.9	531	17 Q97V62	Q97V62 sulfolobus
62	33	56.9	703	12 Q83467	Q83467 porcine ade
63	33	56.9	725	5 Q9VD08	Q9VD08 drosophila
64	33	56.9	821	16 Q9RXG4	Q9RXG4 deinococcus
65	33	56.9	842	17 Q970B4	Q970B4 sulfolobus
66	33	56.9	1021	5 Q15733	Q15733 dictyosteli
67	33	56.9	1063	4 Q8TDZ7	Q8TDZ7 homo sapien
68	33	56.9	1235	16 Q929A9	Q929A9 listeria in
69	33	56.9	1235	16 Q8Y511	Q8Y511 listeria mo
70	33	56.9	1824	5 Q9U0Y5	Q9U0Y5 leishmania
71	32	55.2	61	10 Q8S6G8	Q8S6G8 oryza sativ
72	32	55.2	132	8 Q956K0	Q956K0 rhodotorula
73	32	55.2	136	16 Q8XFN0	Q8XFN0 salmonella
74	32	55.2	143	12 Q9WT48	Q9WT48 human herpe
75	32	55.2	143	12 Q9DYD9	Q9DYD9 human herpe

OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 6803;
 RA Tabata S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugilura M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugilura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D64001; BAA10324.1; ...
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 333 AA; 37436 MW; 676E7399E4499ED6 CRC64;

Query Match 70.7%; Score 41; DB 16; Length 333;
 Best Local Similarity 77.8%; Pred. No. 6.5;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 DB 172 TVVYPTLVF 180
 |||||:|

RESULT 2
 ID 001574 PRELIMINARY; PRT; 974 AA.
 AC 001574;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 111.6 kDa protein.
 GN F48Cl.1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Gattung S., Le T.T.;
 RT "The sequence of C. elegans cosmid F48Cl.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;

RT "Direct Submission.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97015; AAB52345.1; ...
 DR InterPro; IPR000602; Glyco_hydro_38.
 DR Pfam; PF01074; Glyco_hydro_38; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 974 AA; 111586 MW; C825EFA33FB2F964 CRC64;

Query Match 70.7%; Score 41; DB 5; Length 974;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
 DB 851 QTIYPPPMF 860
 :||| |||

RESULT 3
 ID 09CIU3 PRELIMINARY; PRT; 394 AA.
 AC 09CIU3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ABC transporter ATP binding protein.
 GN YCGB OR LL0263.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Balotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 lactis ssp. lactis Il1403.";
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006263; AAK04361.1; ...
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABCtransportr.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 394 AA; 43946 MW; 2822CBC28AEA4C36 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 394;
 Best Local Similarity 66.7%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 DB 47 TLIYPTMRF 55
 :||| |||

RESULT 4
 ID 08VWX1 PRELIMINARY; PRT; 390 AA.
 AC 08VWX1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Delta-15 desaturase.
 GN FAD3.
 OS Perilla frutescens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.

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OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. OKDONG: TISSUE=DEVELOPING SEED;
RA Kim K.-H., Hwang S.-K., Hwang Y.-S.;
RT "Cloning of Perilla delta-15 desaturase.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213482; AAL36934.1; -
DR InterPro: IPR001225; FA.desaturase.
DR Pfam: PF00487; FA.desaturase; 1.
DR ProDom: PD001081; FA.desaturase; 2.
SQ SEQUENCE 390 AA; 44857 MW; 6959C941D47A15AB CRC64;

Query Match 63.8%; Score 37; DB 10; Length 390;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMFK 11
Db 241 TIVGPNMMFK 250

RESULT 5
Q9ZPP7
ID Q9ZPP7 PRELIMINARY; PRT; 391 AA.
AC Q9ZPP7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Omega-3 fatty acid desaturase.
GN FAD3.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUWON-8;
RX MEDLINE=99205707; PubMed=10189709;
RA Chung C.-H., Kim J.-L., Lee Y.-C., Choi Y.-L.;
RT "Cloning and characterization of a seed-specific omega-3 fatty acid
desaturase cDNA from Perilla frutescens.";
RL Plant Cell Physiol. 40:114-118(1999).
DR EMBL; AF047039; AAD15744.1; -
DR InterPro: IPR001225; FA.desaturase.
DR Pfam: PF00487; FA.desaturase; 1.
DR ProDom: PD001081; FA.desaturase; 2.
SQ SEQUENCE 391 AA; 44931 MW; 6637E81654C17CEC CRC64;

Query Match 63.8%; Score 37; DB 10; Length 391;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMFK 11
Db 242 TIVGPNMMFK 251

RESULT 6
Q912X4
ID Q912X4 PRELIMINARY; PRT; 395 AA.
AC Q912X4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA1765.
DN PA1765.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004602; AAG05154.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 395 AA; 44670 MW; FC183A433B2529C8 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 395;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
Db 292 RQVYPSLLF 301

RESULT 7
Q9LUC5
ID Q9LUC5 PRELIMINARY; PRT; 512 AA.
AC Q9LUC5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Putative cytochrome P450 protein).
GN MIEL20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banno J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Jones T.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Kim C.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MIEL20 (GI:9294391).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AB023038; BAB02401.1; -
DR EMBL; AY050827; AAK92762.1; -
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS; PR00385; P450.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 512 AA; 58442 MW; 19DDEAD9C9BAF0B CRC64;

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Query Match 62.1%; Score 36; DB 10; Length 512;
 Best Local Similarity 63.6%; Pred. No. 90;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
 I : I I I I I
 DB 80 RVVYPLQMF 90

RESULT 8

Q9FX69 ID Q9FX69 PRELIMINARY; PRT; 180 AA.
 AC Q9FX69
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE T6J4.4 protein.
 GN T6J4.4
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
 RA Buehler E., Chao Q., Chin Q., Chlou J., Choi E., Gonzalez A.,
 RA Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
 RA Lenz C., Liu A., Liu S., Mukharasy N., Pham P., Sakano H., Shinn P.,
 RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC011810; AAG09557.1; -
 SQ SEQUENCE 180 AA; 19794 MW; 5DA0943DB333F332 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 180;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
 I : I I I I I
 DB 124 RQLVPTKLF 133

RESULT 9

Q93ZC5 ID Q93ZC5 PRELIMINARY; PRT; 254 AA.
 AC Q93ZC5
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Atlg13280/T6J4.23.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY057636; AAL15267.1; -
 SQ SEQUENCE 254 AA; 27809 MW; 4D82FA4889242353 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 254;
 Best Local Similarity 60.0%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
 I : I I I I I
 DB 198 RQLVPTKLF 207

RESULT 10

Q9LS01 ID Q9LS01 PRELIMINARY; PRT; 258 AA.
 AC Q9LS01
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Genomic DNA, chromosome 3, TAC clone:K13N2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.,
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 DR EMBL; AB028607; BAA95765.1; -
 SQ SEQUENCE 258 AA; 28398 MW; 42AF942E0E9AAB87 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 258;
 Best Local Similarity 60.0%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
 I : I I I I I
 DB 202 RQLVPTKLF 211

RESULT 11

Q8ZLZ1 ID Q8ZLZ1 PRELIMINARY; PRT; 264 AA.
 AC Q8ZLZ1
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative arylsulfate sulfotransferase.
 GN STM3192.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OC NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SCSCI412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";

RL Nature 413:852-856(2001).
 DR EMBL; AE008846; AAL22066.1; -
 KW Transferase; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 264 AA; 29462 MW; 2B3F39791813620F CRC64;

Query Match 60.3%; Score 35; DB 16; Length 264;
 Best Local Similarity 66.7%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMFK 11

||:||||

256 LVHPTQMF 264

RESULT 12

Q94JV3

ID Q94JV3 PRELIMINARY; PRT; 282 AA.

AC Q94JV3;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE AT5g46920/MQD22.6.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,

RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,

RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,

RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,

RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,

RA Davis R.W., Southwick A., Ecker J.R.;

RT "Arabidopsis cdna clones."

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF372919; AAK49635.1; -

DR InterPro; IPR000442; Intron_maturase2.

DR Pfam; PF01348; Intron_maturase2; 1.

SQ SEQUENCE 282 AA; 32875 MW; 89B0C6FFA2ABF4B8 CRC64;

Query Match

Best Local Similarity 60.3%; Score 35; DB 10; Length 282;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 10

|||||:

9 RRVVYPTLRY 18

RESULT 13

Q8VGS2

ID Q8VGS2 PRELIMINARY; PRT; 320 AA.

AC Q8VGS2;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Olfactory receptor MOR187-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;

RT "The olfactory receptor gene superfamily of the mouse."

RL Nat. Neurosci. 0:0-0(2002).

RN [2]

RP SEQUENCE FROM N.A.

RA Adams M.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY073074; AAL60737.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODPSN
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 320 AA; 36768 MW; 1FF2EBF1413280F1 CRC64;

Query Match 60.3%; Score 35; DB 11; Length 320;

Best Local Similarity 75.0%; Pred. No. 89;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMM 9

||:||||

82 TVIYPKMM 89

RESULT 14

Q9WZ16

ID Q9WZ16 PRELIMINARY; PRT; 435 AA.

AC Q9WZ16;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE PMSA-related protein.

GN TM0727.

OS Thermotoga maritima.

OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

OX NCBI_TaxID=2336;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109;

RA MEDLINE=9287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

RT "Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima."

RL Nature 399:323-329(1999).

DR EMBL; AE001743; AAD35809.1; -

DR TIGR; TM0727; -

DR InterPro; IPR002510; PmbA_TlDD.

DR Pfam; PF01523; PmbA_TlDD; 1.

KW Complete proteome.

SQ SEQUENCE 435 AA; 48306 MW; C8764A342A975819 CRC64;

Query Match

Best Local Similarity 54.5%; Score 35; DB 16; Length 435;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11

||:||||

135 RVVWVPTVMYK 145

RESULT 15

Q9EME6

ID Q9EME6 PRELIMINARY; PRT; 504 AA.

AC Q9EME6;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE AMV260.

GN AMV260.

OS Ansacta moorei entomopoxvirus (AmEPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;

OC Entomopoxvirus B.

OX NCBI_TaxID=28321;

RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094;
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete Genomic Sequence of the Ansacta moorei Entomopoxvirus:
RT Analysis and Comparison with Other Poxviruses.";
RL Virology 274:120-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF250284; AAG02966.1; -;
SQ SEQUENCE 504 AA; 61862 MW; ACA9BFFA559FAA50 CRC64;

Query Match 60.3%; Score 35; DB 12; Length 504;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
Db 459 TVIPTSLLFR 468

RESULT 16
Q823N6 PRELIMINARY; PRT; 598 AA.
ID Q823N6
AC Q823N6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Probable arylsulfate sulfotransferase.
GN SY3370.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
RC MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor T.,
RA Cronin A., Davis P., Davies K.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL627278; CAB07717.1; -;
KW Transferase; Complete proteome.
SQ SEQUENCE 598 AA; 66586 MW; B5434F028A5421F0 CRC64;

Query Match 60.3%; Score 35; DB 16; Length 598;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMFK 11
Db 590 LVHPTQMF 598

RESULT 17
Q8SWA5 PRELIMINARY; PRT; 705 AA.
ID Q8SWA5
AC Q8SWA5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein ECU02_1230.

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GN ECU02_1230.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=GB-M1;
RC MEDLINE=21576510; PubMed=11719806;
RA Ratinka M.D., Duprat S., Cornillot E., Metenier G., Thamarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL: AL590442; CAD25152.1; -;
KW Hypothetical protein.
SQ SEQUENCE 705 AA; 79649 MW; 235B834A40258AEF CRC64;

Query Match 60.3%; Score 35; DB 5; Length 705;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMM 9
Db 570 TVIYPTLL 577

RESULT 18
Q8S7E2 PRELIMINARY; PRT; 733 AA.
ID Q8S7E2
AC Q8S7E2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 82.3 kDa protein.
GN OSJNBA0057121.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsiirir T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA Vanaken S.E., Utterback T.R., Feldblum T.V., Kaib E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA0057121 genomic sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC087599; AAL79699.1; -;
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82297 MW; 24C8521E18220D9D CRC64;

Query Match 60.3%; Score 35; DB 10; Length 733;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
Db 462 RRVYPTLLR 471

RESULT 19
Q9FJR9 PRELIMINARY; PRT; 735 AA.
ID Q9FJR9

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AC Q9FJR9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Similarity to maturase-related protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:203-216(1998).
DR EMBL; AB013394; BAB10231.1; -
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 735 AA; 85179 MW; 3C4A940CDA6E1590 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 735;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
DB 462 RRVYPTLRY 471

RESULT 20
Q92VV2
ID Q92VV2 PRELIMINARY; PRT; 887 AA.
AC Q92VV2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE T5A14.3 protein.
GN T5A14.3
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Lueros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005223; AAD10640.1; -
DR HSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 887 AA; 99904 MW; 748B215B02E9E9BC CRC64;

Query Match 60.3%; Score 35; DB 10; Length 887;
Best Local Similarity 70.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 11
DB 696 TVVNPMLMLK 705

RESULT 21
Q9HFO9
ID Q9HFO9 PRELIMINARY; PRT; 1030 AA.
AC Q9HFO9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chitinase.
DE Chitinase.
GN CHIC.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FGSC 4;
RA Specht C.A., Benfield B.B., Garcia J.J.;
RT "Identification of bacteria-like chitinases in fungi.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314225; AAG34171.1; -
DR HSSP; P10968; 2CWG.
DR InterPro; IPR001579; Chitinase_18/2.
DR InterPro; IPR001002; Chitin_binding_1.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF00187; Chitin_bind_1; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR ProDom; PD000609; Chitin_binding_1; 1.
DR SMART; SM00270; ChEBD1; 2.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 1030 AA; 112748 MW; 8EE1E64192AF03E5 CRC64;

Query Match 60.3%; Score 35; DB 3; Length 1030;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
DB 951 TVVYPTLTF 959

RESULT 22
Q84121
ID Q84121 PRELIMINARY; PRT; 54 AA.
AC Q84121;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Influenza A/Shearwater/Australia/75 (H5N3), neuraminidase (Seg 6), 5'
DE end (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017869; PubMed=6927853;
RA Blok J., Air G.M.;
RT "Sequence variation at the 3' end of the neuraminidase gene from 39
RT influenza type A viruses.";
RL Virology 121:211-229(1982).
DR EMBL; K01014; AAA43416.1; -
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 5916 MW; B0BD49BBF05D0153 CRC64;

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Query Match      58.6%; Score 34; DB 12; Length 54;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPTM 8
DB 43 QTVVYPTI 50

RESULT 23
Q8UUZ6 PRELIMINARY; PRT; 173 AA.
AC Q8UUZ6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alpha A crystallin.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio;
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LENS;
RA Runkle S., Hill J., Kantorow M., Horwitz J., Posner M.;
RT "Cloning and characterization of zebrafish (danio rerio) alpha A-
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY035778; AAK61363.1;
DR InterPro; IPR001436; Crystallin_alpha.
DR InterPro; IPR003090; Crystallin_N.
DR InterPro; IPR002068; Hsp20.
DR Pfam; PF00525; crystallin; 1.
DR Pfam; PF00011; HSP20; 1.
DR PRINTS; PR00299; ACRYSTALLIN.
DR ProDom; PD001193; Crystallin_N; 1.
DR PROSITE; PS01031; HSP20; 1.
SQ SEQUENCE 173 AA; 19714 MW; 301D743DB91BBC13 CRC64;

Query Match      58.6%; Score 34; DB 13; Length 173;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTM 10
DB 12 RTLGYPTRLF 21

RESULT 24
Q98ID0 PRELIMINARY; PRT; 180 AA.
AC Q98ID0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein mll2459.
GN MLL2459.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
```

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RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL: AP002999; BAB49586.1;
DR InterPro; IPR005149; PAdr.
DR Pfam; PF03551; PAdr; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 180 AA; 19909 MW; D94F736B2855CF60 CRC64;

Query Match      58.6%; Score 34; DB 16; Length 180;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
DB 49 VVYPTLTF 56

RESULT 25
Q8XNC4 PRELIMINARY; PRT; 212 AA.
AC Q8XNC4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CPE0414.
GN CPE0414.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RL flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AP003186; BAB80120.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 212 AA; 24363 MW; DB7E1E2AC94BE697 CRC64;

Query Match      58.6%; Score 34; DB 16; Length 212;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVYPTMMFK 11
DB 205 IYPNMIFK 212

Search completed: July 16, 2003, 14:37:07
Job time : 45 secs
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 44.3333 Seconds
(without alignments)
33.062 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	65.5	207	11 AAG29277	Arabidopsis thalia
2	38	65.5	262	18 AAW27262	Plant steroid 5-al
3	38	65.5	262	21 AAG29276	Arabidopsis thalia
4	38	65.5	394	23 ABB53569	Lactococcus lactis
5	37	63.8	560	22 ABB53569	Novel human diagno
6	36	62.1	82	22 AAO10186	Human polypeptide
7	35	60.3	242	21 AAG09307	Arabidopsis thalia
8	35	60.3	244	21 AAG07361	Arabidopsis thalia
9	35	60.3	244	21 AAG61263	Arabidopsis thalia
10	35	60.3	246	21 AAY32315	Soybean neutral tr

11	35	60.3	251	21 AAG07360	Arabidopsis thalia
12	35	60.3	251	21 AAG61262	Arabidopsis thalia
13	35	60.3	252	21 AAG09306	Arabidopsis thalia
14	35	60.3	254	21 AAG09305	Arabidopsis thalia
15	35	60.3	254	22 AAB86353	A. thaliana aliene
16	35	60.3	254	23 ABB90980	Herbicidally activ
17	35	60.3	258	21 AAG07359	Arabidopsis thalia
18	35	60.3	258	21 AAG61261	Arabidopsis thalia
19	34	58.6	56	21 AAG55171	Arabidopsis thalia
20	34	58.6	56	21 AAG50760	Arabidopsis thalia
21	34	58.6	57	21 AAG55170	Arabidopsis thalia
22	34	58.6	57	21 AAG50759	Arabidopsis thalia
23	34	58.6	264	21 AAG05880	Arabidopsis thalia
24	34	58.6	264	21 AAG51213	Arabidopsis thalia
25	34	58.6	264	22 AAW78329	Human protein SEQ
26	34	58.6	266	21 AAG51212	Arabidopsis thalia
27	34	58.6	267	21 AAG05879	Arabidopsis thalia
28	34	58.6	322	20 AAY30161	Human dorsal root
29	34	58.6	322	20 AAY30162	Human dorsal root
30	34	58.6	322	22 AAEL2794	Human G protein co
31	34	58.6	322	22 AAU04371	Human GTP-binding
32	34	58.6	322	22 AAG54294	Human MrgX1 (mas-r
33	34	58.6	322	23 AAEL2188	Human G-protein co
34	34	58.6	322	23 AAEL17074	Rhinocladiaella atr
35	34	58.6	591	21 AAY58905	Rhinocladiaella atr
36	34	58.6	598	21 AAY58903	Rhinocladiaella atr
37	33	57.8	1810	22 ABB71194	Drosophila melanog
38	33	56.9	99	23 ABB41643	Human ovarian anti
39	33	56.9	310	21 AAB21021	Human nucleic acid
40	33	56.9	593	22 AAU51414	Propionibacterium
41	33	56.9	609	20 AAW82726	Adenovirus PACTSs1
42	33	56.9	609	20 AAW82727	Adenovirus P1q4KN
43	33	56.9	656	22 AAG50823	C glutamic prote
44	33	56.9	700	22 AAB28610	Yeast Rf1. Uniden
45	33	56.9	725	22 AAB86884	Drosophila melanog
46	33	56.9	750	20 AAW82728	Adenovirus PNP51g4
47	33	56.9	1235	23 ABB48680	Listeria monocytog
48	32	55.2	66	22 AAU55532	Propionibacterium
49	32	55.2	72	23 ABB33743	Human ORF2716 prot
50	32	55.2	74	23 AAO21674	Human secreted pro
51	32	55.2	93	22 AAW83247	Human immune/haema
52	32	55.2	137	22 AAU45923	Propionibacterium
53	32	55.2	156	22 AAU65539	Propionibacterium
54	32	55.2	283	23 ABB49253	Listeria monocytog
55	32	55.2	358	23 AAM52346	Hydrtase-aldorase
56	32	55.2	445	20 AAY42113	Corn anthranilate
57	32	55.2	447	22 AAU03135	Streptococcus pyog
58	32	55.2	447	22 AAU03140	Streptococcus pyog
59	32	55.2	447	23 ABB30002	Streptococcus poly
60	32	55.2	462	21 AAY58906	Amino polyol amine
61	32	55.2	462	21 AAY58907	Amino polyol amine
62	32	55.2	462	21 AAY68843	Amino acid sequenc
63	32	55.2	462	21 AAY68844	Amino acid sequenc
64	32	55.2	463	21 AAY58909	Amino polyol amine
65	32	55.2	463	21 AAY68845	Amino acid sequenc
66	32	55.2	487	21 AAY58912	Amino polyol amine
67	32	55.2	487	21 AAY68848	An aminopolyol ami
68	32	55.2	491	20 AAY41302	Tobacco anthranila
69	32	55.2	519	23 ABB27100	Streptococcus poly
70	32	55.2	526	23 ABB92684	Herbicidally activ
71	32	55.2	554	21 AAY58910	Amino polyol amine
72	32	55.2	554	21 AAY68846	An aminopolyol ami
73	32	55.2	577	20 AAW93815	Rice ASA first iso
74	32	55.2	577	20 AAW93810	Rice anthranilate
75	32	55.2	595	23 ABB93363	Herbicidally activ

ALIGNMENTS

RESULT 1
AAG29277
ID AAG29277 standard; Protein: 207 AA.

PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
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 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
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 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.5%; Score 38; DB 21; Length 207;
 Best Local Similarity 45.5%; Pred. NO. 9.2;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVVPTMMFK 11
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 Db 38 RTIIYPLRLFR 48

RESULT 2

AAW27262
 ID AAW27262 standard; Protein; 262 AA.

XX AC AAW27262;

XX DT 23-APR-1998 (first entry)

XX DE Plant steroid 5-alpha reductase DET2.
 XX

KW Plant steroid 5-alpha reductase; Arabidopsis; DET2; pest resistance;
 KW brassinolide biosynthesis; growth.
 XX Arabidopsis sp.
 OS Arabidopsis sp.
 PN WO9739112-A1.
 PD 23-OCT-1997.
 XX 14-APR-1997; 97WO-US06115.
 XX 18-APR-1996; 96US-0634475.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Chory J, Li J;
 XX WPI; 1997-526449/48.
 DR N-PSDB; AAT91260.
 XX New isolated plant steroid 5-alpha reductase gene, DET2 - used to
 PT develop products for e.g. increasing plant yield and pest resistance
 PT or for producing plants with reduced stature
 XX Claim 4; Page 45-46; 70pp; English.
 XX The present sequence represents a novel plant steroid 5-alpha reductase,
 CC DET2. Methods have also been developed for producing plants with
 CC increased yield, as compared to wild-type. The DET2 polypeptides have
 CC SAR activity and are involved in the brassinolide biosynthesis pathway.
 CC The products and methods can be used to produce modified plants which
 CC can exhibit increased plant growth, increased crop yield or increased
 CC biomass. The plants can also have increased resistance to pests and
 CC pesticides. Inhibitors of DET2 can be used to cause loss of function of
 CC DET2 resulting in, e.g. male sterile plants or reduced stature (dwarf
 CC plants).
 XX SQ Sequence 262 AA:
 Query Match 65.5%; Score 38; DB 18; Length 262;
 Best Local Similarity 45.5%; Pred. NO. 12;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RTVVVPTMMFK 11
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 Db 93 RTIIYPLRLFR 103
 RESULT 3
 AAG29276
 ID AAG29276 standard; Protein; 262 AA.
 XX AC AAG29276;
 XX 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 34805.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 XX PD 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 01-JUN-1999; 99US-0136782.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
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PR 28-JUL-1999; 99US-0145951.
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PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 23-AUG-1999; 99US-0149902.
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PR 27-AUG-1999; 99US-0151066.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158233.
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PR 14-OCT-1999; 99US-0159638.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 65.5%; Score 38; DB 21; Length 262;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMMFK 11
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Db 93 RTIIVPLRLR 103

RESULT 4

ABB53569
ID ABB53569 standard; Protein; 394 AA.

XX AC ABB53569;

XX DT 16-MAY-2002 (first entry)

XX DE Lactococcus lactis protein ycgB.

XX KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

XX OS Lactococcus lactis IL1403.

XX PN FR2807446-Al.

XX PD 12-OCT-2001.

XX PF 11-APR-2000; 2000FR-0004630.

XX PR 11-APR-2000; 2000FR-0004630.

XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX DR WPI; 2002-043418/06.

XX PT New nucleotide sequence useful in the identification or Lactococcus
lactis and related species -

PS Claim 6; SEQ ID No 271; 2504pp; French.

XX

CC The present invention is related to a Lactococcus lactis nucleotide
sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
nucleic acid sequence is useful in the detection and/or amplification of
nucleic acid sequence, particularly to identify Lactococcus lactis or
related species. The proteins of the invention are useful for the
biosynthesis or biodegradation of a composition of interest. The
invention helps research in lactic bacteria, particularly useful in the
production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
WO2001/77334 (published 18-OCT-2001) which is available in electronic
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 394 AA;

Query Match 65.5%; Score 38; DB 23; Length 394;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
:::|::|:
Db 47 TLIYPTMRF 55

RESULT 5

ABG29423
ID ABG29423 standard; Protein; 560 AA.

XX AC ABG29423;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #29414.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO2001/75067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS93610.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity -

XX PS Claim 20; SEQ ID No 59782; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC. and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 560 AA;

Query Match 63.88; Score 37; DB 22; Length 560;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVPTMMF 10
Db 214 TLVPTMMF 222
I: I I I I I I I I I I

RESULT 6
AAO10186
ID AAO10186 standard; Protein; 82 AA.

AC AAO10186;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 24078.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI90117.

Isolated nucleic acids and polypeptides, useful for preventing
diagnosing and treating e.g. leukaemia, inflammation and immune
disorders.

Claim 20; SEQ ID NO 24078; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 7187.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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Query Match 60.3%; Score 35; DB 21; Length 244;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
I : : : : :
Db 188 RQLVYPTKLF 197

RESULT 10
AAY32315
ID AAY32315 standard; Protein; 246 AA.
XX
AC AAY32315;
XX
DT 28-FEB-2000 (first entry)

XX Soybean neutral triacylglycerol lipase.
DE
XX
KW Triacylglycerol lipase; soybean; fatty acid; seed oil;
KW vegetable oil; transgenic plant.
XX
XX Glycine max.
OS
XX
PN W09955883-A2.
XX
PD 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-US09280.
PF
XX 30-APR-1998; 98US-0083688.
XX
FA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Cahoon EB, Cahoon RE, Kinney AJ, Rafalski JA;
PI
XX WPI: 2000-062036/05.
XX
DR N-PSDB; AAZ34964.
DR
XX Novel plant triacylglycerol lipase polynucleotides used to alter the
PT level of the enzyme in transgenic plants -
PT
XX Claim 10; Page 58-59; 65pp; English.
PS
XX This sequence represents most of a soybean neutral triacylglycerol
CC lipase (TAGL), as deduced from the nucleotide sequence of isolated
CC cDNA clones (see AAZ34964). Novel acid and neutral TAGL polypeptides
CC (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,
CC Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes
CC may be prepared recombinantly and used to raise antibodies, which
CC are used for detecting the enzymes in situ in cells or in vitro in
CC cell extracts. The polynucleotides may be used to create transgenic
CC plants in which the TAGL levels are present at higher or lower levels
CC than normal, or in cell types or developmental processes where they are
CC not normally found. This would alter the level of triacylglycerol and
CC cholesterol esters found in those cells. Accumulation of fatty acids
CC with unusual structures may be a positive phenotype in plants used for
CC foods. In addition, it may be desirable to eliminate expression of TAGL
CC genes for certain applications. TAGL enzymes may also be useful for the
CC processing of plant seed oils and for the development of novel seed
CC oils. The TAGL enzymes can also be used as targets to facilitate the
CC design and/or identification of inhibitors of those enzymes that may be
CC useful as herbicides. This is desirable because inhibition of the
CC activity of either of the enzymes could lead to an inhibition of plant
CC growth.
XX
SQ Sequence 246 AA;

Query Match 60.3%; Score 35; DB 21; Length 246;
Best Local Similarity 62.5%; Pred. NO. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
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DB 75 ILYPTIMP 82

RESULT 11
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ID AAG07360 standard; Protein; 251 AA.
XX
AC AAG07360;
XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 4484.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW

KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
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Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 195 RQLVYPTKLF 204

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ID AAG61262 standard; Protein; 251 AA.
XX
AC AAG61262;

DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79442.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.
XX
PN EP1033405-A2.

XX 06-SEP-2000.
PD

XX 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825.
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Best Local Similarity 60.08; Pred. No. 47;
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XX 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 7186.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX XX
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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Query Match 60.3%; Score 35; DB 21; Length 252;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 196 RQLVPTKLF 205

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XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 7185.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX XX 25-FEB-2000; 2000EP-0301439.

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Query Match 60.3%; Score 35; DB 21; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
DB 198 RQLVYPTKLF 207

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RESULT 15
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ID AAB86353 standard; Protein; 254 AA.
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DT 20-SEP-2001 (first entry)
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DE A. thaliana allene oxide cyclase protein SEQ ID 10.
XX
KW Allene oxide cyclase; jasmonic acid; plant; AOC; jasmonate biosynthesis;
KW signalling molecule; gene expression; stress response; perfume synthesis;
KW wound-induced signal cascade; defensive response; transgenic plant;
KW protease inhibitor synthesis; phytoalexin synthesis; alkaloid synthesis;
KW pathogen resistance; herbicide resistance; ultra-violet protection;
KW secondary metabolite production; male sterility; flower development;
KW seed formation; germination.
XX
OS Arabidopsis thaliana.
XX
PN WO200157224-A2.
XX
PD 09-AUG-2001.
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PF 02-FEB-2001; 2001WO-EP01148.
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PR 02-FEB-2000; 2000DE-1004468.
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PI Ziegler J, Stenzel I, Hause B, Wasternack C;
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WPI; 2001-483438/52.
DR N-PSDB; AAB21490.
XX
PT Nucleic acid encoding plant allene oxide cyclase, useful for producing
PT transgenic plants with altered jasmonic acid synthesis, e.g. increased
PT resistance to pathogens -
XX
PS Claim 1b; Page 55-56; 66pp; German.

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XX This invention describes novel nucleic acids (I), encoding proteins
CC (II) with the activity of the allene oxide cyclase (AOC) involved in
CC jasmonate biosynthesis. Jasmonic acid (JA) is a signalling molecule
CC involved in: (i) altered gene expression in plants in response to
CC stress; and (ii) developmental processes. It is also an intermediate in
CC the wound-induced signal cascade and induces many defensive responses in
CC plants, including synthesis of protease inhibitors, phytoalexins,
CC alkaloids and perfumes. (I) is used: (i) to produce transgenic plants,
CC cells etc. with altered AOC activity, specifically altered resistance to
CC pathogens and herbivores, optimal plant/useful insect/pest interaction;
CC increased biomass, altered carbohydrate and nitrogen metabolism;
CC and/or phytoalexins, optimal secondary metabolites (especially alkaloids
CC sterility and/or altered development, especially flower development, seed
CC formation and/or germination; (ii) for selective production of 9S/13S
CC (cis(+))-12-oxophytodienoic acid (III), a precursor of jasmonic acid
CC (JA); (iii) for isolation of homologous sequences; and (iv) to express
CC AOC in prokaryotic or eukaryotic cells or (in antisense orientation) to
CC inhibit its expression. (I) Makes possible large scale production of high
CC purity JA. (I) is very specific for production of (III) (contrast
CC non-enzymatic methods which produce mixtures of isomers) which is a
CC precursor for the natural enantiomer of JA. This sequence represents the
CC Arabidopsis thaliana AOC described in the invention.
XX
SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 22; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
DB 198 RQLVYPTKLF 207

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| : |||| : |

RESULT 16
ABB90980
ID ABB90980 standard; Protein; 254 AA.
XX ABB90980;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 191.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.
XX
PA (FARB ) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 191; 261pp + Sequence Listing; English.
XX
The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 28-OCT-1999; 99US-0161993.
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Query Match 60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RTVVYPTMMF 10
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Db 202 RQLVYPTKLF 211
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AC AAG61261;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 79441.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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PR	20-AUG-1999;	99US-0149929.	XX	AC	99US-0126785.
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AAG60760 standard; Protein; 56 AA.

AAG60760;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 78740.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 14-OCT-1999; 99US-0159638.
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PR 22-OCT-1999; 99US-0160981.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.6%; Score 34; DB 21; Length 57;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 29 KLIVPTROYK 39

RESULT 23

AAG05880
ID AAG05880 standard; Protein; 264 AA.

XX AC AAG05880;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 2450.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 21-APR-1999; 99US-0130449.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.6%; Score 34; DB 21; Length 264;

Best Local Similarity 75.0%; Pred. No. 79; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1;

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Db 106 VVYPAVMF 113

RESULT 25

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ID AAW78329 standard; Protein; 264 AA.

XX AC AAW78329;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 991.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US04098.

XX PR 03-FEB-2000; 2000US-0496914.

XX PR 27-APR-2000; 2000US-0560875.

XX PR 20-JUN-2000; 2000US-0598075.

XX PR 19-JUL-2000; 2000US-0620325.

XX PR 01-SEP-2000; 2000US-0654936.

XX PR 15-SEP-2000; 2000US-0663561.

XX PR 20-OCT-2000; 2000US-0693325.

XX PR 30-NOV-2000; 2000US-0728422.

XX PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI; 2001-476283/51.
 DR N-PSDB; AAK51462.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 3215-3216; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 SQ Sequence 264 AA;

Query Match 58.6%; Score 34; DB 22; Length 264;
 Best Local Similarity 62.5%; Pred. NO. 79;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
 Db :||| |||
 97 ILYPVMMF 104

Search completed: July 16, 2003, 14:33:11
 Job time : 44.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:31:07 ; Search time 15 seconds
(without alignments)
21.577 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	65.5	246	US-08-634-475-3	Sequence 3, Appli
2	38	65.5	246	US-09-709-791-3	Sequence 3, Appli
3	38	65.5	262	US-08-634-475-2	Sequence 2, Appli
4	38	65.5	262	US-09-709-791-2	Sequence 2, Appli
5	34	58.6	591	US-09-352-159-46	Sequence 46, Appli
6	34	58.6	598	US-09-352-159-42	Sequence 42, Appli
7	33	56.9	700	US-08-274-121B-5	Sequence 5, Appli
8	32	55.2	462	US-09-352-159-6	Sequence 6, Appli
9	32	55.2	462	US-09-352-159-8	Sequence 8, Appli
10	32	55.2	462	US-09-352-168-6	Sequence 6, Appli
11	32	55.2	462	US-09-352-168-8	Sequence 8, Appli
12	32	55.2	463	US-09-352-159-11	Sequence 11, Appli
13	32	55.2	463	US-09-352-168-11	Sequence 11, Appli
14	32	55.2	468	US-08-959-011-3	Sequence 3, Appli
15	32	55.2	487	US-09-352-159-21	Sequence 21, Appli
16	32	55.2	487	US-09-352-168-21	Sequence 21, Appli
17	32	55.2	491	US-09-001-826-23	Sequence 23, Appli
18	32	55.2	554	US-09-352-159-17	Sequence 17, Appli
19	32	55.2	554	US-09-352-168-17	Sequence 17, Appli
20	32	55.2	577	US-09-486-382B-2	Sequence 2, Appli
21	32	55.2	577	US-09-486-382B-13	Sequence 13, Appli
22	32	55.2	595	US-08-604-789B-3	Sequence 3, Appli
23	32	55.2	595	US-09-312-721A-3	Sequence 3, Appli
24	32	55.2	598	US-09-352-159-40	Sequence 40, Appli
25	32	55.2	600	US-09-352-159-23	Sequence 23, Appli
26	32	55.2	600	US-09-352-159-36	Sequence 36, Appli
27	32	55.2	600	US-09-352-159-38	Sequence 38, Appli

28	32	55.2	600	4	US-09-352-168-23	Sequence 23, Appli
29	32	55.2	692	4	US-09-352-159-19	Sequence 19, Appli
30	32	55.2	692	4	US-09-352-168-19	Sequence 19, Appli
31	32	55.2	829	4	US-09-352-159-33	Sequence 33, Appli
32	32	55.2	829	4	US-09-352-168-33	Sequence 33, Appli
33	32	55.2	991	4	US-09-352-159-27	Sequence 27, Appli
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35	32	55.2	1000	4	US-09-352-159-25	Sequence 25, Appli
36	32	55.2	1000	4	US-09-352-168-25	Sequence 25, Appli
37	32	55.2	1196	4	US-09-352-159-31	Sequence 31, Appli
38	32	55.2	1196	4	US-09-352-168-31	Sequence 31, Appli
39	32	55.2	1205	4	US-09-352-159-29	Sequence 29, Appli
40	32	55.2	1205	4	US-09-352-168-29	Sequence 29, Appli
41	31	53.4	125	2	US-08-408-095-35	Sequence 35, Appli
42	31	53.4	149	4	US-09-134-001C-2957	Sequence 2957, Ap
43	31	53.4	201	2	US-08-933-750C-21	Sequence 21, Appli
44	31	53.4	201	2	US-09-234-613-21	Sequence 21, Appli
45	31	53.4	320	2	US-08-933-750C-12	Sequence 12, Appli
46	31	53.4	320	4	US-09-234-613-12	Sequence 12, Appli
47	31	53.4	535	4	US-09-269-731-4	Sequence 4, Appli
48	31	53.4	1487	2	US-08-760-489-2	Sequence 2, Appli
49	31	53.4	1487	2	US-08-760-489-4	Sequence 2, Appli
50	31	53.4	1487	4	US-09-185-373-2	Sequence 2, Appli
51	31	53.4	1487	4	US-09-185-373-4	Sequence 4, Appli
52	31	53.4	3011	3	US-08-811-566-20	Sequence 20, Appli
53	31	53.4	3011	4	US-09-014-416-1	Sequence 1, Appli
54	31	53.4	3011	4	US-09-014-416-5	Sequence 5, Appli
55	31	53.4	3011	4	US-09-034-756-20	Sequence 20, Appli
56	31	53.4	3012	3	US-08-811-566-2	Sequence 2, Appli
57	31	53.4	3012	4	US-09-034-756-2	Sequence 2, Appli
58	30.5	52.6	371	4	US-09-574-141A-56	Patent No. 5182210
59	30	51.7	280	6	5182210-12	Sequence 4, Appli
60	30	51.7	451	1	US-08-625-322-4	Sequence 13, Appli
61	30	51.7	490	2	US-08-673-789-13	Sequence 4, Appli
62	30	51.7	621	3	US-08-604-789B-4	Sequence 4, Appli
63	30	51.7	621	4	US-09-312-721A-4	Sequence 4, Appli
64	30	51.7	697	2	US-08-674-351-4	Sequence 2, Appli
65	30	51.7	701	4	US-09-132-028-2	Sequence 2, Appli
66	30	51.7	722	4	US-09-134-001C-5482	Sequence 5482, Ap
67	30	51.7	744	1	US-08-162-809-20	Sequence 20, Appli
68	30	51.7	1437	3	US-09-061-400-2	Sequence 2, Appli
69	30	51.7	1453	2	US-09-001-273-2	Sequence 2, Appli
70	30	51.7	1453	4	US-08-843-459A-2	Sequence 2, Appli
71	29	50.0	17	4	US-09-227-357-426	Sequence 426, App
72	29	50.0	68	4	US-09-097-889-17	Sequence 17, Appl
73	29	50.0	156	4	US-09-134-001C-4450	Sequence 4450, Ap
74	29	50.0	305	4	US-08-858-207A-392	Sequence 392, App
75	29	50.0	401	4	US-09-134-001C-4403	Sequence 4403, Ap

ALIGNMENTS

RESULT 1
US-08-634-475-3
; Sequence 3, Application US/08634475
; Patent No. 6143950
; GENERAL INFORMATION:
; APPLICANT: Chory et al., Joanne
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
; TITLE OF INVENTION: DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,475
FILING DATE: 18-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/015001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-634-475-3

Query Match 65.5%; Score 38; DB 4; Length 246;
Best Local Similarity 45.5%; Pred. No. 8.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
Db 77 RTIIYPLRLFR 87

RESULT 2

US-09-709-791-3
Sequence 3, Application US/09709791
Patent No. 6352846

GENERAL INFORMATION:
APPLICANT: Chory, Joanne
Li, Jianming

TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
DET2

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th floor
CITY: Newport Beach
STATE: CA

COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/709,791
FILING DATE: 07-NOV-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: SALKINS.010DVI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/235-8550

TELEFAX: 619/235-0176

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-709-791-3

Query Match 65.5%; Score 38; DB 4; Length 246;
Best Local Similarity 45.5%; Pred. No. 8.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
Db 77 RTIIYPLRLFR 87

RESULT 3

US-08-634-475-2

Sequence 2, Application US/08634475

Patent No. 6143950

GENERAL INFORMATION:

APPLICANT: Chory et al., Joanne

TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,

TITLE OF INVENTION: DET2

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/634,475

FILING DATE: 18-APR-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07251/015001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-634-475-2

Query Match 65.5%; Score 38; DB 4; Length 262;
Best Local Similarity 45.5%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
Db 93 RTIIYPLRLFR 103

RESULT 4

US-09-709-791-2

Sequence 2, Application US/09709791

Patent No. 6352846

GENERAL INFORMATION:

APPLICANT: Chory, Joanne

Li, Jianming

TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP

STREET: 620 Newport Center Drive, 16th floor

CITY: Newport Beach

DET2

STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Duwick, Jonathan P.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/709,791
FILING DATE: 07-NOV-93
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: SALKINS.010DV1
TELEPHONE: 619/235-8550
TELEFAX: 619/235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-709-791-2

Query Match 65.5%; Score 38; DB 4; Length 262;
Best Local Similarity 45.5%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 11
|::||:|:
DB 93 RTIYPLRL 103

RESULT 5
US-09-352-159-46
; Sequence 46, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rhinocycladiella atrovirens
US-09-352-159-46

Query Match 58.6%; Score 34; DB 4; Length 591;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:||||:
DB 405 TTYPTLIF 413

RESULT 6

US-09-352-159-42
; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Rhinocycladiella atrovirens
US-09-352-159-42

Query Match 58.6%; Score 34; DB 4; Length 598;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:||||:
DB 406 TTYPTLIF 414

RESULT 7
US-08-274-121B-5
; Sequence 5, Application US/08274121B
; Patent No. 6133034
; GENERAL INFORMATION:
; APPLICANT: Arne Reider Strom
; APPLICANT: Inga Kaasen
; APPLICANT: Olaf Bay Styrvold
; APPLICANT: John McDougall
; TITLE OF INVENTION: Methods and Compositions
; TITLE OF INVENTION: Related To The Production
; TITLE OF INVENTION: of Trehalose
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,121B
; FILING DATE: 12-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/893,099
; FILING DATE: 27-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 86(1)
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-274-121B-5

Query Match 56.9%; Score 33; DB 4; Length 700;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
Db : : : : :
672 KAIYPTFF 681

RESULT 8

US-09-352-159-6
; Sequence 6, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duviack, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-6

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db : : : : :
270 TTLYPPLTF 278

RESULT 9

US-09-352-159-8
; Sequence 8, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duviack, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8

; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-8

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db : : : : :
270 TTLYPPLTF 278

RESULT 10

US-09-352-168-6
; Sequence 6, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duviack, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-6

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db : : : : :
270 TTLYPPLTF 278

RESULT 11

US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duviack, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-8

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db : : : : :
270 TTLYPPLTF 278

US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duviack, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-8

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
Db 270 TTYLPTLTF 278

RESULT 12
US-09-352-159-11
; Sequence 11, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352.159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092.936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135.391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-11

Query Match 55.2%; Score 32; DB 4; Length 463;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
Db 271 TTYLPTLTF 279

RESULT 13
US-09-352-168-11
; Sequence 11, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352.168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092.936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; OTHER INFORMATION: Extra lysine in the polypeptide sequence of
; OTHER INFORMATION: K:RAPAO, 463 aa.
US-09-352-168-11

Query Match 55.2%; Score 32; DB 4; Length 463;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
Db 271 TTYLPTLTF 279

RESULT 14
US-08-959-011-3
; Sequence 3, Application US/08959011
; Patent No. 5932444
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959.011
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0412 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 497984
US-08-959-011-3

Query Match 55.2%; Score 32; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTVVYPTM 8
Db 244 RTVVPTM 251

RESULT 15
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-09-352-159-21

Query Match 55.2%; Score 32; DB 4; Length 487;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 295 TTYLPTLTF 303

RESULT 16
US-09-352-168-21
; Sequence 21, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:TRAPAO translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature TRAPAO in maize.
US-09-352-168-21

Query Match 55.2%; Score 32; DB 4; Length 487;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 295 TTYLPTLTF 303

RESULT 17
US-09-001-826-23
; Sequence 23, Application US/09001826A
; Patent No. 5965727
; GENERAL INFORMATION:

; APPLICANT: SONG, HEE-SOOK
; APPLICANT: BROTHERTON, JEFFREY E.
; APPLICANT: WIDHOLM, JACK M.
; TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
; FILE REFERENCE: U001.C1
; CURRENT APPLICATION NUMBER: US/09/001,826A
; CURRENT FILING DATE: 1997-12-31
; EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
; EARLIER FILING DATE: 1997-07-25; 1996-07-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO 23
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-001-826-23

Query Match 55.2%; Score 32; DB 2; Length 491;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
I :|||: I
Db 422 RTIVPPT 428

RESULT 18
US-09-352-159-17
; Sequence 17, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
US-09-352-159-17

Query Match 55.2%; Score 32; DB 4; Length 554;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
I :|||: I
Db 362 TTYLPTLTF 370

RESULT 19
US-09-352-168-17
; Sequence 17, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.

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; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352.168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
; OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-352-168-17

Query Match          55.2%; Score 32; DB 4; Length 554;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  2  TVVYPTMMF 10
    I :|||: I
Db  362  TTYLPTLTF 370

RESULT 20
US-09-486-382B-2
; Sequence 2, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
; APPLICANT: Hokko Chemical Industry Co., Ltd.
; APPLICANT: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
; TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
; FILE REFERENCE: 10647
; CURRENT APPLICATION NUMBER: US/09/486.382B
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: JP 9-235049
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-486-382B-2

Query Match          55.2%; Score 32; DB 4; Length 577;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  1  RTVVVYPT 7
    ||:|:|
Db  508  RTIVFPT 514

RESULT 21
US-09-486-382B-13
; Sequence 13, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
; APPLICANT: Hokko Chemical Industry Co., Ltd.
; APPLICANT: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
; TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
; FILE REFERENCE: 10647
; CURRENT APPLICATION NUMBER: US/09/486.382B
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: JP 9-235049
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; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified amino acid sequence of Sequence No. 6388174 2
; Patent No. 6388174
US-09-486-382B-13

Query Match          55.2%; Score 32; DB 4; Length 577;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  1  RTVVVYPT 7
    ||:|:|
Db  508  RTIVFPT 514

RESULT 22
US-08-604-789B-3
; Sequence 3, Application US/08604789B
; Patent No. 6118047
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,789B
; FILING DATE: 19-Jan-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-604-789B-3

Query Match          55.2%; Score 32; DB 3; Length 595;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db      526 RTIVPT 532

RESULT 23
US-09-312-721A-3
; Sequence 3, Application US/09312721A
; Patent No. 6271016
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwesman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,721A
; FILING DATE: 17-May-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,789
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.0260S2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-312-721A-3
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Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVVYPT 7
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Db      526 RTIVPT 532

RESULT 24
US-09-352-159-40
; Sequence 40, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; US-09-352-159-23

Query Match      55.2%; Score 32; DB 4; Length 600;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
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Db      406 TTLVPTLTF 416

RESULT 25
US-09-352-159-23
; Sequence 23, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; US-09-352-159-23

Query Match      55.2%; Score 32; DB 4; Length 598;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
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Db      406 TTLVPTLTF 416

RESULT 26
US-09-352-159-23
; Sequence 23, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; US-09-352-159-23

Query Match      55.2%; Score 32; DB 4; Length 600;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
      |:|:|:|
Db      408 TTLVPTLTF 416

Search completed: July 16, 2003, 14:38:03
Job time : 15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:33:19 ; Search time 27.6667 Seconds
(without alignments)
47.218 Million cell updates/sec

Title: US-09-923-716c-2
Perfect score: 58
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Searched: 451899 seqs, 118759770 residues

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Post-processing: Minimum Match 0%
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Database : Published Applications_AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	34	58.6	600	9	US-10-183-116-16
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6	34	58.6	600	9	US-10-183-116-16
7	34	58.6	600	9	US-10-183-116-16
8	34	58.6	600	9	US-10-183-116-16
9	34	58.6	600	9	US-10-183-116-16
10	34	58.6	600	9	US-10-183-116-16
11	33	56.9	600	9	US-10-183-116-16
12	33	56.9	656	9	US-09-738-626-4577
13	32	55.2	447	9	US-10-169-048-34
14	32	55.2	447	9	US-10-169-048-34
15	32	55.2	462	9	US-09-770-564-8
16	32	55.2	462	9	US-09-770-564-8
17	32	55.2	463	9	US-10-183-116-16
18	32	55.2	463	9	US-10-183-116-16
19	32	55.2	463	9	US-10-183-116-16

20	32	55.2	463	9	US-10-072-307-50	Sequence 50, Appl
21	32	55.2	463	9	US-09-770-564-11	Sequence 11, Appl
22	32	55.2	487	9	US-09-770-564-21	Sequence 21, Appl
23	32	55.2	539	9	US-10-072-307-34	Sequence 34, Appl
24	32	55.2	554	9	US-09-770-564-17	Sequence 17, Appl
25	32	55.2	595	10	US-09-733-300-3	Sequence 3, Appl1
26	32	55.2	600	9	US-10-072-307-26	Sequence 26, Appl
27	32	55.2	600	9	US-10-072-307-27	Sequence 27, Appl
28	32	55.2	600	9	US-10-072-307-29	Sequence 29, Appl
29	32	55.2	600	9	US-10-072-307-31	Sequence 31, Appl
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33	32	55.2	600	9	US-10-072-307-38	Sequence 38, Appl
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36	32	55.2	600	9	US-10-072-307-44	Sequence 44, Appl
37	32	55.2	600	9	US-10-072-307-45	Sequence 45, Appl
38	32	55.2	600	9	US-10-072-307-52	Sequence 52, Appl
39	32	55.2	600	9	US-10-072-307-54	Sequence 54, Appl
40	32	55.2	600	9	US-10-072-307-56	Sequence 56, Appl
41	32	55.2	600	9	US-10-072-307-58	Sequence 58, Appl
42	32	55.2	600	9	US-10-072-307-66	Sequence 66, Appl
43	32	55.2	600	9	US-09-770-564-23	Sequence 23, Appl
44	32	55.2	692	9	US-09-770-564-19	Sequence 19, Appl
45	32	55.2	829	9	US-09-770-564-33	Sequence 33, Appl
46	32	55.2	991	9	US-09-770-564-27	Sequence 27, Appl
47	32	55.2	1000	9	US-09-770-564-25	Sequence 25, Appl
48	32	55.2	1196	9	US-09-770-564-31	Sequence 31, Appl
49	32	55.2	1205	9	US-09-770-564-29	Sequence 29, Appl
50	31	53.4	57	10	US-09-864-761-47860	Sequence 47860, A
51	31	53.4	58	9	US-09-764-891-2918	Sequence 2918, Ap
52	31	53.4	157	9	US-09-992-598-103	Sequence 103, App
53	31	53.4	157	9	US-09-989-233A-103	Sequence 103, App
54	31	53.4	157	9	US-09-989-735-103	Sequence 103, App
55	31	53.4	157	9	US-09-989-444-103	Sequence 103, App
56	31	53.4	157	9	US-09-989-730-103	Sequence 103, App
57	31	53.4	157	9	US-09-990-436-103	Sequence 103, App
58	31	53.4	157	9	US-09-991-181-103	Sequence 103, App
59	31	53.4	157	9	US-09-993-687-103	Sequence 103, App
60	31	53.4	157	9	US-09-989-734-103	Sequence 103, App
61	31	53.4	157	9	US-09-997-653-103	Sequence 103, App
62	31	53.4	157	9	US-10-174-590-90	Sequence 90, Appl
63	31	53.4	157	9	US-10-176-758-90	Sequence 90, Appl
64	31	53.4	157	9	US-10-175-737-90	Sequence 90, Appl
65	31	53.4	157	9	US-09-993-667-103	Sequence 103, App
66	31	53.4	157	9	US-10-173-706-90	Sequence 90, Appl
67	31	53.4	157	9	US-10-175-738-90	Sequence 90, Appl
68	31	53.4	157	9	US-10-175-752-90	Sequence 90, Appl
69	31	53.4	157	9	US-10-176-482-90	Sequence 90, Appl
70	31	53.4	157	9	US-10-176-757-90	Sequence 90, Appl
71	31	53.4	157	9	US-10-176-913-90	Sequence 90, Appl
72	31	53.4	157	9	US-10-180-552-90	Sequence 90, Appl
73	31	53.4	157	9	US-10-180-557-90	Sequence 90, Appl
74	31	53.4	157	9	US-09-990-438-103	Sequence 103, App
75	31	53.4	157	9	US-09-990-562-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-10-183-116-16
; Sequence 16, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4CICPI

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; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-16

Query Match
Best Local Similarity 58.6%; Score 34; DB 9; Length 322;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
Db 97 ILYPVMMF 104

RESULT 2
US-10-079-384-4
; Sequence 4, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-4

Query Match
Best Local Similarity 58.6%; Score 34; DB 9; Length 322;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
Db 97 ILYPVMMF 104

RESULT 3
US-10-072-307-28
; Sequence 28, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
```

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; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 28
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_F7
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-28

Query Match
Best Local Similarity 58.6%; Score 34; DB 9; Length 600;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db 408 TTYPTLIF 416

RESULT 4
US-10-072-307-30
; Sequence 30, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 30
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G11
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-30

Query Match
Best Local Similarity 58.6%; Score 34; DB 9; Length 600;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db 408 TTYPTLIF 416

RESULT 5
US-10-072-307-35
; Sequence 35, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
```

; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 35
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F15C3
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-35

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :||||:|
Db 408 TTYPTLIF 416

RESULT 6
US-10-072-307-37
; Sequence 37, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 37
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F19F2
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-37

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :||||:|
Db 408 TTYPTLIF 416

RESULT 7
US-10-072-307-40
; Sequence 40, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 40
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F24F2
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-40

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :||||:|
Db 408 TTYPTLIF 416

RESULT 8
US-10-072-307-43
; Sequence 43, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 43
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F3B5
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-43

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :||||:|
Db 408 TTYPTLIF 416

RESULT 9
US-10-072-307-60
; Sequence 60, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 60

; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocladiaella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 215
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 216
; OTHER INFORMATION: Xaa = Gln, His
US-10-072-307-60

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||:|
Db 408 TTLYPTLIF 416

RESULT 10
US-10-072-307-64
; Sequence 64, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2002-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocladiaella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 13
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 403
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 404
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 419
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 433
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 443
; OTHER INFORMATION: Xaa = Ter, Cys, Trp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 478
; OTHER INFORMATION: Xaa = Leu, Ter, Ser, Trp
; FEATURE:
; NAME/KEY: unsure

; LOCATION: 489
; OTHER INFORMATION: Xaa = Ter, Arg, Gly
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 538
; OTHER INFORMATION: Xaa = Ter, Arg, Gly
US-10-072-307-64

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||:|
Db 408 TTLYPTLIF 416

RESULT 11
US-10-072-307-62
; Sequence 62, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2002-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocladiaella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 187
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 209
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 244
; OTHER INFORMATION: Xaa = Glu, Asp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 262
; OTHER INFORMATION: Xaa = Ter, Cys, Trp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 295
; OTHER INFORMATION: Xaa = Tyr, Asn, Asp, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 299
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 403
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 405
; OTHER INFORMATION: Xaa = Ala, Thr, Pro, Ser
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 409

; OTHER INFORMATION: Xaa = Ala, Thr, Ser, Pro
US-10-072-307-62

Query Match 56.9%; Score 33; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
I :|||:
Db 408 TXLYPTLIF 416

RESULT 12

US-09-738-626-4577
; Sequence 4577, Application US/09738626
; Publication No. US20020197605A1

GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4577
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4577

Query Match 56.9%; Score 33; DB 9; Length 656;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMF 10
I :|||:
Db 307 IIMPTMMF 314

RESULT 13

US-10-169-048-34
; Sequence 34, Application US/10169048
; Publication No. US20030072769A1

GENERAL INFORMATION:

; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Their Use
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34

; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-34

Query Match 55.2%; Score 32; DB 9; Length 447;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
I :|||:
Db 190 QTIYPTTFK 200

RESULT 14

US-10-169-048-44
; Sequence 44, Application US/10169048
; Publication No. US20030072769A1

GENERAL INFORMATION:

; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-44

Query Match 55.2%; Score 32; DB 9; Length 447;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
I :|||:
Db 190 QTIYPTTFK 200

RESULT 15

US-09-770-564-6
; Sequence 6, Application US/09770564
; Publication No. US20030126636A1

GENERAL INFORMATION:

; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-770-564-6

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 270 TTYLPTLTF 278

RESULT 16
US-09-770-564-8
; Sequence 8, Application US/09770564
; Publication No. US20030126638A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: Polynucleotides and Related Polypeptides and Methods of Use
; CURRENT APPLICATION NUMBER: US 09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 1999-07-12
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-770-564-8

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 270 TTYLPTLTF 278

RESULT 17
US-10-072-307-46
; Sequence 46, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 46
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_TrH1
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-46

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTYLPTLTF 279

RESULT 18
US-10-072-307-47
; Sequence 47, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 47
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G6
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-47

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTYLPTLTF 279

RESULT 19
US-10-072-307-48
; Sequence 48, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 48
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_H8
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-48

Query Match 55.2%; Score 32; DB 9; Length 463;

Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|
Db 271 TTYLPTLTF 279

RESULT 20

US-10-072-307-50
; Sequence 50, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072.307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 50
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_B6
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-50

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|
Db 271 TTYLPTLTF 279

RESULT 21

US-09-770-564-11
; Sequence 11, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770.564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; OTHER INFORMATION: Extra lysine in the polypeptide sequence of
; OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-770-564-11

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|
Db 271 TTYLPTLTF 279

RESULT 22

US-09-770-564-21
; Sequence 21, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770.564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-770-564-21

Query Match 55.2%; Score 32; DB 9; Length 487;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|
Db 295 TTYLPTLTF 303

RESULT 23

US-10-072-307-34
; Sequence 34, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072.307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 34
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4Fl5A11
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-34

Query Match          55.2%; Score 32; DB 9; Length 539;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
      | :|||: |
Db      347 TTLYPTLTF 355

RESULT 24
US-09-770-564-17
; Sequence 17, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
; OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-770-564-17

Query Match          55.2%; Score 32; DB 9; Length 554;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
      | :|||: |
Db      362 TTLYPTLTF 370

RESULT 25
US-09-733-300-3
; Sequence 3, Application US/09733300
; Patent No. US20020061570A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; APPLICANT: Chomet, P.S.
; APPLICANT: Griffor, M.C.
; APPLICANT: Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/09/733,300
; FILING DATE: 08-Dec-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,721
; FILING DATE: 2000-09-11
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-733-300-3

Query Match          55.2%; Score 32; DB 10; Length 595;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVVYPT 7
      | :|||: |
Db      526 RTIVPT 532

Search completed: July 16, 2003, 14:39:39
Job time : 27.6667 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 20 Seconds
(without alignments)
52.874 Million cell updates/sec

Title: US-09-923-716c-2
Perfect score: 58
Sequence: 1 RTVVYPTMFK 11

Scoring table: - BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	333	2 S74406	hypothetical prote
2	41	70.7	974	2 T29545	hypothetical prote
3	38	65.5	262	2 C84800	3-oxo-5-alpha-ster
4	38	65.5	394	2 G86657	ABC transporter AT
5	37	63.8	395	2 H83424	hypothetical prote
6	35	60.3	180	2 D86267	T6J4.4 protein - A
7	35	60.3	435	2 E72342	pmbA-related prote
8	35	60.3	598	2 AG0890	probable arylsulfa
9	35	60.3	887	2 B96598	hypothetical prote
10	34	58.6	303	2 H84758	hypothetical prote
11	34	58.6	347	2 AD3513	channel protein vi
12	34	58.6	373	2 S17955	long-chain-fatty-a
13	34	58.6	373	2 S15161	long-chain-fatty-a
14	34	58.6	389	2 AD0478	acetylornithine de
15	34	58.6	404	2 B41317	O-antigen ligase c
16	34	58.6	404	2 A80973	O-antigen ligase (
17	34	58.6	464	2 T50785	nucleoid DNA-bind
18	34	58.6	674	2 D72329	hypothetical prote
19	34	58.6	711	2 A86424	unknown protein, 3
20	33.5	57.8	1724	2 T13942	UNC-13-B protein -
21	33	56.9	120	1 E69798	conserved hypotet
22	33	56.9	136	2 A90710	regulator of nucle
23	33	56.9	136	2 E85560	regulator of nucle
24	33	56.9	136	2 I57917	nucleoside diphosp
25	33	56.9	205	2 S29308	hypothetical prote
26	33	56.9	205	2 F83013	probable transcrip
27	33	56.9	221	2 AH0324	probable transcrip
28	33	56.9	261	2 T05447	hypothetical prote
29	33	56.9	390	2 AF3425	oxidoreductase (EC

ALIGNMENTS

RESULT 1

S74406
hypothetical protein sl10456 - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S74406

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74406

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-333 <KAN>

A:Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAAL0324.1; PID:d101

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 70.7%; Score 41; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 2.8;

hypothetical prote
hypothetical prote
glutamyl-tRNA synt
hypothetical prote
ATP-dependent prote
hypothetical prote
ATP-dependent deox
photosystem II pro
regulator of nucle
7,8-dihydro-8-oxog
transcription regu
transactivator (im
lipopolysaccharide
proteolnase inhibit
conserved hypotet
hypothetical prote
hypothetical prote
hypothetical prote
maturase-like prot
hypothetical prote
hypothetical prote
immediate-early pr
hypothetical prote
glutamate/aspartat
polyA polymerase (E
vacuolar ATPase (E
hypothetical prote
anthranilate synth
hypothetical prote
hypothetical prote
anthranilate synth
NADH2 dehydrogenas
hypothetical prote
probable DNA-direc
ribulose-bisphosph
probable DNA-direc
genome polyprotein
hypothetical prote
Na+/H+ antiporter
hypothetical prote
hypothetical prote
MUTR/nudix family
hypothetical prote
hypothetical prote
hypothetical prote

33 56.9 394 2 S69870
33 56.9 531 2 D90453
33 56.9 551 2 D69282
33 56.9 594 2 S00961
33 56.9 821 2 B75530
33 56.9 1021 2 T08601
33 56.9 1235 2 AC1358
33 56.9 1235 2 AC1728
32 55.2 61 1 F2RZKS
32 55.2 136 2 AC0578
32 55.2 142 2 G98072
32 55.2 143 1 WMBE6H
32 55.2 143 2 T43976
32 55.2 169 2 S72166
32 55.2 201 2 T07011
32 55.2 203 2 E75413
32 55.2 214 2 G71318
32 55.2 214 2 D89985
32 55.2 214 2 T49174
32 55.2 283 2 T13879
32 55.2 283 2 AG1560
32 55.2 283 2 A11202
32 55.2 285 2 T09308
32 55.2 334 2 T44163
32 55.2 421 2 S26246
32 55.2 458 2 A96938
32 55.2 468 2 A55116
32 55.2 513 2 T40998
32 55.2 526 2 T49199
32 55.2 543 2 T22585
32 55.2 564 2 S15962
32 55.2 595 2 J01684
32 55.2 603 2 T11843
32 55.2 620 2 T21391
32 55.2 1416 2 D71350
32 55.2 1501 2 T29094
32 55.2 1716 2 T14103
32 55.2 3175 1 REWVEV
31 53.4 80 2 A60450
31 53.4 95 2 B83814
31 53.4 104 2 T17649
31 53.4 105 2 T44098
31 53.4 142 2 G95207
31 53.4 185 2 T29063
31 53.4 207 2 D65095
31 53.4 207 2 A98123

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|||||:::|
Db 172 TWVPTLVF 180

RESULT 2

T29545

hypothetical protein F48C1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29545

R:Gatung, S.; Le, T.T.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid F48C1.

A:Reference number: Z20638

A:Accession: T29545

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-974 <GAT>

A:Cross-references: EMBL:U97015; PIDN:AAB52345.1; GSPDB:GN00019; CESP:F48C1.1

A:Experimental source: strain Bristol N2; clone F48C1

C:Genetics:

A:Map position: 1

A:Gene: CESP:F48C1.1

A:Introns: 15/2; 58/3; 110/3; 150/1; 176/1; 267/2; 296/2; 326/2; 394/3; 441/1; 550/3; 59

Query Match

Best Local Similarity 70.7%; Score 41; DB 2; Length 974;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10

:|::||| |||

Db 851 QTIYPPMMF 860

RESULT 3

C84800

3-oxo-5-alpha-steroid 4-dehydrogenase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: C84800

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nicrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84800

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-262 <STO>

A:Cross-references: GB:AE002093; NID:g4895180; PIDN:AAD32767.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g38050

A:Map position: 2

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match

Best Local Similarity 65.5%; Score 38; DB 2; Length 262;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 11

:|::||| ::|

Db 93 RTIYPLRLR 103

RESULT 4

G85657

ABC transporter ATP binding protein ycgB [imported] - Lactococcus lactis subsp. lactis

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: G86657

R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G86657

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <STO>

A:Cross-references: GB:AE005176; PID:g12723123; PIDN:AAK04361.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: YcgB

Query Match

Best Local Similarity 65.5%; Score 38; DB 2; Length 394;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10

:|::||| |

Db 47 TLIYPTMRF 55

RESULT 5

H83424

hypothetical protein PA1765 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83424

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83424

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <STO>

A:Cross-references: GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG05154.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1765

Query Match

Best Local Similarity 63.8%; Score 37; DB 2; Length 395;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10

:|::||| ::|

Db 292 ROVVYPSLLF 301

RESULT 6

D86267

T6J4.4 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001

C:Accession: D86267

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maith, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86267

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <STO>
A:Cross-references: GB:AE005172; NID:g9958068; PIDN:AAG09557.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 180;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
|:|||||:
Db 124 ROLVPTTKLF 133

RESULT 7

pmbA-related protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72342
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72342

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-435 <ARN>

A:Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
A:Experimental source: strain MSB8
C:Genetics:

A:Gene: TM0727

C:Superfamily: Escherichia coli pmbA protein

Query Match 60.3%; Score 35; DB 2; Length 435;
Best Local Similarity 54.5%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
|:|:|:|:
Db 135 RVVVPVTMYK 145

RESULT 8

AG0890
probable arylsulfate sulfotransferase [imported] - Salmonella enterica subsp. enterica s
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0890

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608

A:Accession: AG0890

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-598 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD07717.1; PID:g16504269; GSPDB:GN00176
C:Genetics:

A:Gene: STY3370

Query Match 60.3%; Score 35; DB 2; Length 598;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMFK 11
:|:|:|:|

Db 590 LVHPTQMEK 598

RESULT 9

B96598
hypothetical protein T5A14.3 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B96598

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96598

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-887 <STO>

A:Cross-references: GB:AE005173; NID:g4204259; PIDN:AAD10640.1; GSPDB:GN00141

C:Genetics:

A:Gene: T5A14.3

A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 887;
Best Local Similarity 70.0%; Pred. No. 1.le+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
||| ||:|:
Db 696 TVVNTMLK 705

RESULT 10

H84758
hypothetical protein At2g34620 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84758

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84758

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303 <STO>

A:Cross-references: GB:AE002093; NID:g3128213; PIDN:AAC26693.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g34620

A:Map position: 2

Query Match 58.6%; Score 34; DB 2; Length 303;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
||:|:|:
Db 120 RTLYPVFMF.129

RESULT 11

AD3513
channel protein virB6 homolog [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AD3513
 R:DeIvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, P.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AD3513
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <KUR>
 A:Cross-references: GB:AE008918; PIDN:AAL53271.1; PID:g17984152; GSPDB:GN00191
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI10030
 A:Map position: II

Query Match 58.6%; Score 34; DB 2; Length 347;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
 I:| | | | |
 Db 257 TVVPMYMK 266

RESULT 12

S17955
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium leiognathi
 C:Species: Photobacterium leiognathi
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
 C:Accession: S17955
 R:Lee, C.Y.; Sztitner, R.B.; Meighen, E.A.
 Eur. J. Biochem. 201, 161-167, 1991
 A:Title: The lux genes of the luminous bacterial symbiont, *Photobacterium leiognathi*, of coll.
 A:Reference number: S17836; MUID:92007870; PMID:1915359
 A:Accession: S17955
 A:Molecule type: DNA
 A:Residues: 1-373 <LEEE>
 A:Cross-references: EMBL:M63594; NID:g150687; PIDN:AAA25620.1; PID:g150692
 C:Genetics:
 A:Gene: luxE
 C:Keywords: acid-thiol ligase
 F;364/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 58.6%; Score 34; DB 2; Length 373;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VYPTMMFK 11
 I:| | | | |
 Db 78 VFPTSMFK 85

RESULT 13

S15161
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium phocae
 N:Alternate names: acyl-protein synthetase
 C:Species: Photobacterium phosphoreum
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C:Accession: S15161
 R:Soly, R.R.; Meighen, E.A.
 J. Mol. Biol. 219, 69-77, 1991
 A:Title: Identification of the acyl transfer site of fatty acyl-protein synthetase from *Photobacterium phocae*
 A:Reference number: S15160; MUID:91218179; PMID:2023262
 A:Accession: S15161
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-373 <JMO>
 C:Genetics:
 A:Gene: luxE
 C:Keywords: acid-thiol ligase
 F;364/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 58.6%; Score 34; DB 2; Length 373;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VYPTMMFK 11
 I:| | | | |
 Db 78 VFPTSMFK 85

RESULT 14

AD0478
 acetylornithine deacetylase (EC 3.5.1.16) [imported] - *Yersinia pestis* (strain CO92)
 C:Species: *Yersinia pestis*
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
 C:Accession: AD0478
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, N.; Nature 413, 523-527, 2001
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AD0478
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-389 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC93392.1; PID:g15981838; GSPDB:GN00175
 C:Genetics:
 A:Gene: argE
 C:Superfamily: succinyl-diaminopimelate desuccinylase
 C:Keywords: hydrolase

Query Match 58.6%; Score 34; DB 2; Length 389;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 I:| | | | |
 Db 238 TIPYPTMMF 246

RESULT 15

B41317
 O-antigen ligase complex protein rfaL - *Salmonella typhimurium*
 C:Species: *Salmonella typhimurium*
 C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
 C:Accession: B41317
 R:MacLachlan, P.R.; Kadam, S.K.; Sanderson, K.E.
 J. Bacteriol. 173, 7151-7163, 1991
 A:Title: Cloning, characterization, and DNA sequence of the rfaL region for lipopolysaccharide synthesis in *Salmonella typhimurium*
 A:Reference number: A41317; MUID:92041612; PMID:1657881
 A:Accession: B41317
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <MAC>
 A:Cross-references: GB:M73826; NID:g154328; PIDN:AAA27206.1; PID:g154330
 C:Keywords: transmembrane protein

Query Match 58.6%; Score 34; DB 2; Length 404;
 Best Local Similarity 63.6%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
 I:| | | | |
 Db 305 RVVDYPTWTFK 315

RESULT 16

AE0973
 O-antigen ligase [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain 09-11-2001)
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C;Accession: AE0973
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant salmonella enterica serovar A;Reference number: AB0502; PMID:11677608
A;Accession: AE0973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <FAR>
A;Cross-references: GB:AL513382; PIDN:CAD03281.1; PID:g16504902; GSPDB:GN00176
C;Genetics:
A;Gene: waaL

Query Match 58.6%; Score 34; DB 2; Length 404;
Best Local Similarity 63.8%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVYPTMMFK 11
| | | | |
Db 305 RVDVPTWTFK 315

RESULT 17
T50785
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50785
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew submitted to the Protein Sequence Database, July 2000
A;Reference number: 225240
A;Accession: T50785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 58/1
A;Note: T30N20_30

Query Match 58.6%; Score 34; DB 2; Length 464;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| | | | |
Db 392 TVTYPTIAF 400

RESULT 18
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72329
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ARN>
A;Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35899.1; PID:g498134
A;Experimental source: strain MSB8

C;Genetics:
A;Gene: TM0817

Query Match 58.6%; Score 34; DB 2; Length 674;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
| | | | |
Db 192 QTFVYVFMF 201

RESULT 19
A86424
unknown protein, 35070-37205 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86424
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marzla Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-711 <STO>
A;Cross-references: GB:AE005172; NID:g10092467; PIDN:AAG12869.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 58.6%; Score 34; DB 2; Length 711;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
| | | | |
Db 461 RRVYPTLRY 470

RESULT 20
T13942
UNC-13-B protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13942
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C. J. Biol. Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic transmission A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13942
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1724 <XUX>
A;Cross-references: EMBL:Y17922; NID:g38931112; PIDN:CAA76942.1; PID:g38931113
C;Genetics:
A;Cross-references: FlyBase:Fbgn0025726
A;Note: UNC-13-B
C;Superfamily: protein kinase C zinc-binding repeat homology
F;602-651/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 57.8%; Score 33.5; DB 2; Length 1724;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 5; Gaps 1;

QY 1 RTVYPTMMF 11
| | | | |

Db 1437 KTIIVPPMTDKTMFK 1452

RESULT 21
E69798
conserved hypothetical protein yeth - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E69798
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choudhury, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallenbach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, K.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69798
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-120 <KUN>
A:CROSS-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12535.1; PID:g2633029
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeth
C:Superfamily: Bacillus probable methylglyoxalase yurT

Query Match 56.9%; Score 33; DB 1; Length 120;
Best Local Similarity 54.5%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 RTVVYPTMFK 11
I I I I I I
Db 53 RLVIYPKAMK 63
I I I I I I
RESULT 22
A90710
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A90710
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99628; MUID:21156231; PMID:11258796
A:Accession: A90710
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <HAY>
A:CROSS-references: GB:BA000007; PIDN:BA034072.1; PID:g13360107; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs0649

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RTVVYPTMM 9
I I I I I I
Db 73 RTLVYPAMK 81
I I I I I I

RESULT 23
E85560

regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85560
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, J.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca, N.; Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <STO>
A:CROSS-references: GB:AE0051174; NID:g12513506; PIDN:AAG54945.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: rnk

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RTVVYPTMM 9
I I I I I I
Db 73 RTLVYPAMK 81
I I I I I I

RESULT 24
I57917

nucleoside diphosphate kinase regulator - Escherichia coli (strain K-12)
N:Alternate names: rnk protein
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 01-Mar-2002
C:Accession: I57917; H64794
R:Schlittman, D.; Shankar, S.; Chakrabarty, A.M.
Mol. Microbiol. 16, 309-320, 1995
A:Title: The Escherichia coli genes sspA and rnk can functionally replace the Pseudomonas reference number: I57917; MUID:96015444; PMID:7565093
A:Accession: I57917
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-136 <RES>
A:CROSS-references: GB:L37900; NID:g598117; PIDN:AAC36933.1; PID:g598118
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:CROSS-references: GB:AE000166; GB:U00096; NID:g1786819; PIDN:AAC73711.1; PID:g17868
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: rnk

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RTVVYPTMM 9
I I I I I I
Db 73 RTLVYPAMK 81
I I I I I I

RESULT 25
S29308

hypothetical protein 3 (phac2 3' region) - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999

C:Accession: S29308; S28380
R:Timm, A.; Steinbuechel, A.
Eur. J. Biochem. 209, 15-30, 1992
A:Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus
A:Reference number: S29303; MUID:93011120; PMID:1396693
A:Accession: S29308
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-205 <TIM>
A:Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47154.1; PID:g45394

Query Match 56.9%; Score 33; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
|||||
Db 172 RTVYQIMM 180

Search completed: July 16, 2003, 14:34:16
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 10.3333 Seconds
(without alignments)
44.152 Million cell updates/sec

Title: US-09-923-716c-2
Perfect score: 58
Sequence: 1 RTVVYPTMFEK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	65.5	262	1 DET2_ARATH	Q38944 arabidopsis
2	34	58.6	373	1 LUXE_PHOLE	P29334 photobacter
3	34	58.6	404	1 RFAL_SALTY	P26471 salmonella
4	33	56.9	136	1 RNK_ECOLI	P40679 escherichia
5	33	56.9	193	1 RCF1_DICDI	O96390 dictyosteli
6	33	56.9	551	1 SYE_ARCFU	O39979 archaeoglob
7	33	56.9	594	1 YAP3_KLULA	P05469 kluyveromyc
8	32	55.2	61	1 PSBK_ORYSA	P12162 oryza sativ
9	32	55.2	61	1 PSBK_WHEAT	P38273 triticum ae
10	32	55.2	143	1 B701_HSV6G	P30024 human herpe
11	32	55.2	169	1 COAD_CHRVI	P71154 chromatium
12	32	55.2	200	1 CAKB_COTJA	Q98855 coturnix co
13	32	55.2	201	1 IP23_LYCES	Q43502 lycopersico
14	32	55.2	214	1 Y473_TREPA	O83486 treponema p
15	32	55.2	421	1 GLUT_BACCA	P24944 bacillus ca
16	32	55.2	468	1 VAS1_BOVIN	P40682 bos taurus
17	32	55.2	595	1 TRPE_ARATH	P32068 arabidopsis
18	32	55.2	603	1 NU5M_HYLLA	P30319 hylobates l
19	32	55.2	1416	1 RPOC_TREPA	O83270 treponema p
20	32	55.2	1716	1 RPAI_RAT	O34889 rattus norv
21	32	55.2	3175	1 RPOA_EAV	P19811 equine arte
22	31	53.4	157	1 SMP1_HUMAN	O95807 homo sapien
23	31	53.4	207	1 YOJ1_ECOLI	Q46872 escherichia
24	31	53.4	320	1 DNC_HUMAN	Q9hc21 homo sapien
25	31	53.4	362	1 MSPL_YEAST	P28737 saccharomyc
26	31	53.4	421	1 GLUT_BACST	P24943 bacillus st
27	31	53.4	437	1 SECY_BUCAI	P57571 buchnera ap
28	31	53.4	439	1 RHG1_HUMAN	Q07960 homo sapien
29	31	53.4	440	1 AK_CHLPN	Q9z610 chlamydia p
30	31	53.4	442	1 SECY_SYNY3	P77964 synecocyst
31	31	53.4	507	1 PDI_DATGL	Q9xf61 datisca glo
32	31	53.4	527	1 KITH_HSVSA	P21293 herpesvirus
33	31	53.4	601	1 NU5M_DASNO	O21335 dasypus nov

34	31	53.4	604	1 NU5M_HORSE	P48656 equus cabal
35	31	53.4	606	1 NU5M_BOVIN	P03920 bos taurus
36	31	53.4	606	1 NU5M_CERSI	O03205 ceratotheri
37	31	53.4	606	1 NU5M_EQUAS	P24485 equus asinu
38	31	53.4	606	1 NU5M_SHEEP	O87556 ovis aries
39	31	53.4	640	1 GIDA_ANASP	Q9yr87 anabaena sp
40	31	53.4	657	1 UVRB_CAMJE	Q9ppm7 campylobact
41	31	53.4	714	1 PBPF_BACSU	P38050 bacillus su
42	31	53.4	1067	1 EG52_XENLA	Q1783 xenopus lae
43	31	53.4	3358	1 PGCY_MOUSE	Q62059 mus musculu
44	31	53.4	4196	1 DFHC_SCHPO	O3290 schizosacch
45	30.5	52.6	1968	1 RRPO_PVMR	P17965 potatou viru
46	30	51.7	61	1 PSBK_HORVU	P19842 photorhabdu
47	30	51.7	116	1 LUXE_PHOLU	P19842 photorhabdu
48	30	51.7	122	1 YJ41_YEAST	Q17121 saccharomyc
49	30	51.7	149	1 YQBN_BACSU	P45930 bacillus su
50	30	51.7	158	1 IP2X_SOLFU	Q00782 solanum tub
51	30	51.7	193	1 RCF2_DICDI	Q99ps3 dictyosteli
52	30	51.7	221	1 KCY1_BORBU	O51154 borrelia bu
53	30	51.7	238	1 YG26_HAEIN	P44278 haemophilus
54	30	51.7	265	1 UL07_HSVSA	Q1028 herpesvirus
55	30	51.7	315	1 VC04_VACCV	P17370 vaccinia vi
56	30	51.7	316	1 VC04_VACCC	P21038 vaccinia vi
57	30	51.7	316	1 VC04_VARU	P34012 variola vir
58	30	51.7	352	1 GLN1_DAUCA	O22504 daucus caro
59	30	51.7	356	1 GLN1_MEDSA	P04078 medicago sa
60	30	51.7	356	1 GLN1_PHAVU	P04770 phaseolus v
61	30	51.7	356	1 GLNA_VIGAC	P32289 vigna aconl
62	30	51.7	358	1 GLNA_LACSA	P3712 lactuca sat
63	30	51.7	376	1 YG3W_YEAST	P32923 saccharomyc
64	30	51.7	378	1 LUXE_VIBHA	P14286 vibrio harv
65	30	51.7	416	1 PXN1_XENLA	P49263 xenopus lae
66	30	51.7	420	1 PUR2_LISIN	Q92ap4 listeria in
67	30	51.7	420	1 PUR2_LISMO	Q8p6c6 listeria mo
68	30	51.7	426	1 STE2_SACKL	P12384 saccharomyc
69	30	51.7	477	1 LYII_HUMAN	Q14108 homo sapien
70	30	51.7	477	1 LYII_RAT	P27615 rattus norv
71	30	51.7	497	1 YJ92_YEAST	P47158 saccharomyc
72	30	51.7	519	1 SNX2_HUMAN	O60749 homo sapien
73	30	51.7	519	1 SNX2_MOUSE	Q9cwk8 mus musculu
74	30	51.7	521	1 PELI_SACPS	P79001 saccharomyc
75	30	51.7	536	1 COA4_DROME	Q9ve00 drosophila

ALIGNMENTS

RESULT 1

DET2_ARATH	DET2_ARATH	STANDARD;	PRT;	262 AA.
ID	DET2_ARATH	STANDARD;	PRT;	262 AA.
AC	Q38944: Q9SH83;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Probable steroid reductase DET2 (EC 1.3.99.-).			
GN	DET2 OR AT2G38050 OR T8P21.4.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OX	eurosid II; Brassicales; Brassicaceae; Arabidopsi.			
NCBI_TaxID	3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	MEDLINE=96183496; PubMed=8602526;			
Li	Li J., Nagpal P., Vitart V., McMorris T.C., Chory J.;			
RT	"A role for brassinosteroids in light-dependent development of			
RT	Arabidopsis.";			
RL	Science 272:398-401(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	MEDLINE=20083487; PubMed=10617197;			

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT SSP consortium full length cDNA clones (RAFLs) sequenced by the
 RT submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Probably involved in a reduction step in the
 CC biosynthesis of the plant steroid, brassinolide. Defects in DET2
 CC leads to defects in light-regulated development.
 CC -1- PATHWAY: Brassinolide biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE STEROID 5-ALPHA REDUCTASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U53860; AAC49264.1; -;
 DR EMBL; AC007661; AAD32767.1; -;
 DR EMBL; AY045926; AAK76600.1; -;
 DR EMBL; AY079337; AAL85068.1; -;
 DR InterPro: IPR001104; Strd5A_dhc.
 DR Pfam: PF02544; Steroid_dh; 1.
 DR PROSITE: PS0244; S5A_REDUCTASE; 1.
 KW Oxidoreductase; Transmembrane.
 FT TRANSMEM 13 33 POTENTIAL.
 FT TRANSMEM 51 71 POTENTIAL.
 FT TRANSMEM 113 133 POTENTIAL.
 FT TRANSMEM 148 168 POTENTIAL.
 FT TRANSMEM 205 225 POTENTIAL.
 FT CONFLICT 198 198 'C' -> 'R' (IN REF. 1).
 SQ SEQUENCE 262 AA; 30635 MW; 88291B8A8AF55664 CRC64;
 Query Match 65.5%; Score 38; DB 1; Length 262;
 Best Local Similarity 45.5%; Pred. No. 1.8;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RTVVYPTMMFK 11
 Db 93 RRIIYPLRLR 103
 RESULT 2
 LUXE_PHOLE
 ID LUXE_PHOLE STANDARD; PRT; 373 AA.
 AC P29334;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase).
 GN LUXE.
 OS Photobacterium leiognathi.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
 OC Photobacterium.
 OX NCBI_TaxID=658;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25521;
 RX MEDLINE=92007870; PubMed=1915359;
 RA Lee C.Y., Szittner R.B., Meighen E.A.;
 RT "The lux genes of the luminous bacterial symbiont, Photobacterium
 RT leiognathi, of the ponyfish. Nucleotide sequence, difference in gene
 RT organization, and high expression in mutant Escherichia coli.";
 RL Eur. J. Biochem. 201:161-167(1991).
 CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -1- CATALYTIC ACTIVITY: App + an acid + protein -> AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -----
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 CC -----
 DR EMBL; M63594; AAA25620.1; -;
 DR PIR; S17955; S17955.
 KW Luminescence; Ligase.
 SQ SEQUENCE 373 AA; 43099 MW; 1B31848B00BF9921 CRC64;
 Query Match 58.6%; Score 34; DB 1; Length 373;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 VYPTMMFK 11
 Db 78 VFPTSMFK 85
 RESULT 3
 RFAL_SALTY
 ID RFAL_SALTY STANDARD; PRT; 404 AA.
 AC P26471;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE O-antigen ligase.
 GN RFAL OR WAAL OR RPBT OR STM3713.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=92041612; PubMed=1657881;
 RA MacLachlan P.R., Kadam S.K., Sanderson K.E.;
 RT "Cloning, characterization, and DNA sequence of the rfaLK region for
 RT lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
 RL J. Bacteriol. 173:7151-7163(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -1- FUNCTION: ADDS THE O-ANTIGEN ON THE GLUCOSE(II) GROUP OF LPS.
 CC -1- PATHWAY: Lipopolysaccharide core biosynthesis.

```
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: SHOWS ALMOST NO SIMILARITY TO E.COLI REAL.
CC -----
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CC -----
DR EMBL; M73826; AAA27206.1; -.
DR EMBL; AE008872; AAL22572.1; -.
DR PIR; B41317; B41317.
DR StyGene; SG10340; rfal.
KW Lipopolysaccharide biosynthesis; Ligase; Transmembrane;
KW Complete proteome.
FT TRANSMEM 66 84 POTENTIAL.
FT TRANSMEM 184 203 POTENTIAL.
FT TRANSMEM 227 244 POTENTIAL.
SQ SEQUENCE 404 AA; 46034 MW; 1B84F7B3C757D2AB CRC64;

Query Match 58.6%; Score 34; DB 1; Length 404;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 RTVVVPTMMFK 11
| | | | |
Db 305 RVDPYPTWTFK 315
| | | | |

RESULT 4
RNK_ECOLI STANDARD; PRT; 136 AA.
AC P40679;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of nucleoside diphosphate kinase.
GN RNK OR B0610 OR 20754 OR ECS0649.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96015444; PubMed=7565093;
RA Schlichtman D., Shankar S., Chakrabarty A.M.;
RT "The Escherichia coli genes sspA and rnk can functionally replace the
RT pseudomonas aeruginosa alginate regulatory gene algR2.";
RL Mol. Microbiol. 16:309-320(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
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```
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA
CC ALGINATE REGULATORY GENE ALGR2.
CC -----
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CC -----
DR EMBL; L37900; AAC36933.1; -.
DR EMBL; AE000166; AAC73711.1; -.
DR EMBL; U82598; AAB40810.1; -.
DR EMBL; D90701; BAA35239.1; -.
DR EMBL; D90702; BAA35248.1; -.
DR EMBL; AE005240; AAG54945.1; -.
DR EMBL; AP002552; BAB34072.1; -.
DR EcoGene; EGI2637; rnk.
KW Complete proteome.
SQ SEQUENCE 136 AA; 14927 MW; 7043926623BA5E1E CRC64;

Query Match 56.9%; Score 33; DB 1; Length 136;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RTVVVPTMM 9
| | | | |
Db 73 RLVYPAMK 81

RESULT 5
RCFL_DICDI
ID RCFL_DICDI STANDARD; PRT; 193 AA.
AC O96390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAS-related protein racfl.
DE RACFL.
GN Dictyostelium discoideum (slime mold).
OS Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
```

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OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214006; PubMed=10198067;
RA Rivero F., Albrecht R., Dislich H., Bracco E., Graciotti L.,
RA Bozzato S., Noegel A.A.;
RT "RacFl", a novel member of the Rho protein family in Dictyostelium
RT discoidium, associates transiently with cell contact areas,
RT macropinosomes and phagosomes."
RL Mol. Biol. Cell 10:1205-1219(1999).
CC CC
CC -1- FUNCTION: MIGHT ACT IN CONCERT AND/OR SHARE FUNCTIONS WITH OTHER
CC MEMBERS OF THE RHO FAMILY IN THE REGULATION OF A SUBSET OF
CC CYTOSKELETAL REARRANGEMENTS THAT ARE REQUIRED FOR THESE PROCESSES.
CC
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC
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CC
DR EMBL: AF037042; AAD09143.1;
DR HSSP: P21181; 1AM4.
DR DictyDb; DD????; racFl.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR001230; Prenyl_site.
DR InterPro; IPR001806; Ras_transfmrng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMS; TIGR00231; small_gtp; 1.
DR GTP-binding; Prenylation; Lipoprotein.
KW NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 115 118 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (POTENTIAL).
FT LIPID 190 190 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 193 AA; 21830 MW; 206E814C823E3B2E CRC64;

Query Match 56.9%; Score 33; DB 1; Length 193;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMFK 11
Db 173 RSVIYPNKLK 183
|:|:|:|:|

RESULT 6
ID SVE_ARCFU STANDARD; PRT; 551 AA.
AC 029979;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (Glurs).
DE GLTX OR AF0260.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

NCBI_TaxID=44689;
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC CC
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
DR EMBL: AE001087; AAB90966.1;
DR HSSP: P00962; 1GTR.
DR TIGR; AF0260;
DR InterPro; IPR004526; GltX_arch.
DR InterPro; IPR000924; Glu_tRNA-synt_lc.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00749; tRNA-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMS; TIGR00463; gltX_arch; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 100 110 "HIGH" REGION.
SQ SEQUENCE 551 AA; 64402 MW; A985A300C6B68F2E CRC64;

Query Match 56.9%; Score 33; DB 1; Length 551;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMFK 11
Db 270 VVYPTLDFE 278
|:|:|:|:|

RESULT 7
ID YKP3_KLULA STANDARD; PRT; 594 AA.
AC P05469;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hypothetical killer plasmid pGKL-2 protein 3.
OS Kluyveromyces lactis (Yeast).
OG Plasmid pGKL-2.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
RX MEDLINE=88289339; PubMed=3041369;
RA Tommasino S., Ricci S., Galeotti C.L.;
RT "Genome organization of the killer plasmid pGKL2 from Kluyveromyces
RT lactis."
RL Nucleic Acids Res. 16:5863-5878(1988).
CC CC
CC -1- FUNCTION: THE PRESENCE OF THE TWO LINEAR PLASMIDS, TERMED
CC PGKL1 AND PGKL2, IN STRAINS OF KLUYVEROMYCES LACTIS CONFERS
CC THE KILLER PHENOTYPE TO THE HOST CELL, BY PROMOTING THE
CC SECRETION OF A TOXIN ABLE TO INHIBIT THE GROWTH OF SENSITIVE

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CC STRAINS.
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CC -----
CC EMBL; X07776; CAA30604.1; -.
CC PIR; S00961; S00961.
CC InterPro; IPR000977; DNA_ligase.
CC Pfam; PF01068; DNA_ligase; 1.
CC KW Hypothetical protein; Plasmid.
CC SQ SEQUENCE 594 AA; 70527 MW; 6AE57D37518BE6B0 CRC64;
CC
CC Query Match 56.9%; Score 33; DB 1; Length 594;
CC Best Local Similarity 36.4%; Pred. No. 45;
CC Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
CC
CC Qy 1 RTVYPTMMFK 11
CC I:|||||:
CC Db 80 RSTMPSLIIF 90
CC
CC RESULT 8
CC PSBK_ORYZA
CC ID PSBK_ORYZA STANDARD; PRT; 61 AA.
CC AC P12162;
CC DT 01-OCT-1989 (Rel. 12, Created)
CC DT 01-OCT-1989 (Rel. 12, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Photosystem II reaction center protein K precursor (PSII-K).
CC GN PSBK.
CC OS Oryza sativa (Rice).
CC OG Chloroplast.
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC OC Ehrhartoideae; Oryzaeae; Oryza.
CC OX NCBI_TaxID=4530;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=cv. Nipponbare; PubMed=2770692;
CC RX MEDLINE=89364698;
CC RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
CC RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
CC RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugliura M.;
CC RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
CC RT intermolecular recombination between distinct trna genes accounts for
CC RT a major plastid DNA inversion during the evolution of the cereals.";
CC RL Mol. Gen. Genet. 217:185-194(1989).
CC RC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC OF PHOTOSYSTEM II.
CC -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC -----
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CC -----
CC EMBL; X15901; CAA34010.1; -.
CC PIR; J00203; F2RZKS.
CC InterPro; IPR003687; PSII_Psbk.
CC Pfam; PF02533; Psbk; 1.
CC KW Photosystem II; Chloroplast.
CC FT PROPEP 1 24 POTENTIAL.
CC FT CHAIN 25 61 PHOTOSYSTEM II REACTION CENTER PROTEIN K.
CC SQ SEQUENCE 61 AA; 6982 MW; BBC361067C4158F5 CRC64;

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Query Match 55.2%; Score 32; DB 1; Length 61;
Best Local Similarity 55.6%; Pred. No. 6.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TVVYPTMMF 10
I:|||||
Db 14 SVIYPTSF 22
I:|||||
I:|||||

RESULT 9
PSBK_WHEAT
ID PSBK_WHEAT STANDARD; PRT; 61 AA.
AC P58273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Photosystem II reaction center protein K precursor (PSII-K).
GN PSBK.
OS Triticum aestivum (Wheat).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA Tsunewaki K.;
RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT complete sequence and contig clones.";
RL Plant Mol. Biol. Rep. 18:243-253(2000).
CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC OF PHOTOSYSTEM II.
CC -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC -----
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CC -----
CC EMBL; AB042240; BAB47017.1; -.
CC DR InterPro; IPR003687; PSII_Psbk.
CC DR Pfam; PF02533; Psbk; 1.
CC KW Photosystem II; Chloroplast.
CC FT PROPEP 1 24 BY SIMILARITY.
CC FT CHAIN 25 61 PHOTOSYSTEM II REACTION CENTER PROTEIN K.
CC SQ SEQUENCE 61 AA; 7030 MW; 467901067C4158FD CRC64;
CC
CC Query Match 55.2%; Score 32; DB 1; Length 61;
CC Best Local Similarity 55.6%; Pred. No. 6.9;
CC Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CC
CC Qy 2 TVVYPTMMF 10
CC I:|||||
CC Db 14 SVIYPTSF 22
CC I:|||||
CC I:|||||

RESULT 10
B701_HSV6G
ID B701_HSV6G STANDARD; PRT; 143 AA.
AC P30024;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein B701.
OS Human herpesvirus (type 6 / strain GS) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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CC Betaherpesvirinae; Roseolovirus.
 OX NCBI_TaxID=10369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92148942; PubMed=1310766;
 RA Geng Y., Chandran B., Josephs S.F., Wood C.;
 RT "Identification and characterization of a human herpesvirus 6 gene 1
 RT segment that trans activates the human immunodeficiency virus type 1
 RT promoter.";
 RL J. Virol. 66:1564-1570(1992).
 CC -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
 CC ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
 CC HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
 CC SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
 CC DIRECTLY OR INDIRECTLY.
 CC -----
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 CC -----
 CC EMBL; M81789; -; NOT_ANNOTATED_CDS.
 DR PIR; A42186; WMBE6H.
 DR Transcription regulation; Trans-acting factor; Activator.
 KW SEQUENCE 143 AA; 16385 MW; D0CB4D7C2422AAD8 CRC64;
 SQ
 Query Match 55.2%; Score 32; DB 1; Length 143;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RTVVYPTMMF 10
 :|::||| |
 Db 50 KTLLYPKTMF 59
 RESULT 11
 COAD_CHRVI
 ID COAD_CHRVI STANDARD; PRT; 169 AA.
 AC P71154;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
 DE phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
 DE pyrophosphorylase).
 GN COAD OR KDTB.
 OS Chromatium vinosum.
 OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
 OC Allochromatium.
 OX NCBI_TaxID=1049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D / ATCC 17899 / DSM 180;
 RX MEDLINE=96328257; PubMed=8765743;
 RA Moulis J.M.;
 RT "Molecular cloning and expression of the gene encoding Chromatium
 RT vinosum 2[4Fe-4S] ferredoxin.";
 RL Biochim. Biophys. Acta 1308:12-14(1996).
 CC -!- FUNCTION: REVERSELY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
 CC PHOSPHOPANTHETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
 CC PYROPHOSPHATE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
 CC dephospho-CoA.
 CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
 CC -!- SUBUNIT: HOMOHETEROMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE COAD FAMILY.
 CC -----
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 CC -----
 CC EMBL; U45327; AAC44332.1; -;
 DR HSSP; P23875; 1B6T.
 DR InterPro; IPR004821; Cyt_tran_rel.
 DR InterPro; IPR004820; Cytidylyltransf.
 DR InterPro; IPR001980; LPS_biosynth.
 DR Pfam; PF01467; Cytidylyltransf; 1.
 DR PRINTS; PR01020; LPSBIOSNTHSS.
 DR TIGRFAMS; TIGR00125; cyt_tran_rel; 1.
 KW Transferase; Nucleotidylyltransferase; Coenzyme A biosynthesis.
 SQ SEQUENCE 169 AA; 18559 MW; 5126FD2BF32824AC CRC64;
 Query Match 55.2%; Score 32; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVVYP 6
 :|:|:|:
 Db 2 RTVVYP 7
 RESULT 12
 CAKB_COTJA
 ID CAKB_COTJA STANDARD; PRT; 200 AA.
 AC Q98855;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative calcium-activated potassium channel beta subunit.
 GN CO6.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224079; PubMed=9070660;
 RA Oberst C., Weiskirchen R., Hartl M., Bister K.;
 RT "Suppression in transformed avian fibroblasts of a gene (CO6)
 RT encoding a membrane protein related to mammalian potassium channel
 RT regulatory subunits.";
 RL Oncogene 14:1109-1116(1997).
 CC -!- FUNCTION: POTASSIUM CHANNEL PROTEIN WHICH MAY MODULATE THE
 CC PROPERTIES OF THE PORE-FORMING ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: THE CALCIUM-ACTIVATED POTASSIUM CHANNEL IS COMPOSED OF
 CC AT LEAST TWO SUBUNITS: A PORE-FORMING ALPHA SUBUNIT AND A
 CC REGULATORY BETA SUBUNIT (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -----
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 CC -----
 CC EMBL; U67865; AAC26967.1; -;
 DR InterPro; IPR003930; BK_channel_beta.
 DR Pfam; PF03185; CakB; 1.
 KW Ionic channel; Transmembrane; Glycoprotein.
 FT TRANSMEM 20 40 POTENTIAL.
 FT TRANSMEM 167 187 POTENTIAL.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 200 AA; 22677 MW; B7A612D8973F711F CRC64;
 Query Match 55.2%; Score 32; DB 1; Length 200;

CC -!- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
CC (SDF, TC 2.A.23).
CC -----
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CC -----
CC EMBL: M85509; AAA22493.1; -.
CC PIR: S26246; S26246.
DR InterPro: IPR001991; Na/dico_symp.
DR Pfam: PF00375; SDF; 1.
DR PROSITE: PS00713; NA_DICARBOXYL_SYMPT_1; 1.
DR PROSITE: PS00714; NA_DICARBOXYL_SYMPT_2; 1.
KW Transport; Transmembrane; Symport.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 24 POTENTIAL.
FT DOMAIN 25 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 POTENTIAL.
FT DOMAIN 65 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 98 POTENTIAL.
FT DOMAIN 99 148 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 149 169 POTENTIAL.
FT DOMAIN 170 198 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 199 219 POTENTIAL.
FT DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 243 POTENTIAL.
FT DOMAIN 244 244 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 245 265 POTENTIAL.
FT DOMAIN 266 306 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 307 327 POTENTIAL.
FT DOMAIN 328 330 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 331 351 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT DOMAIN 373 421 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 421 AA; 45345 MW; 10ABBE12EDD1E7E4 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 421;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VYPTMFM 10
Db 226 VYATMLF 233
||| ||:|

RESULT 16
VAS1_BOVIN STANDARD; PRT; 468 AA.
AC P40682;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14) (V-ATPase S1
DE subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit).
GN ATP6P1 OR ATP6S1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 378-388.
RC TISSUE=Adrenal chromaffin;
RX MEDLINE=95014142; PubMed=7929063;
RA Supek F., Supekova L., Mandiyan S., Pan Y.-C.E., Nelson H., Nelson N.;
RT "A novel accessory subunit for vacuolar H(+)-ATPase from chromaffin
RT granules".
RL J. Biol. Chem. 269:24102-24106(1994).
CC -!- FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY

CC OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -!- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC -----
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CC -----
CC EMBL: U10039; AAA50752.1; -.
KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 468 VACUOLAR ATP SYNTHASE SUBUNIT S1.
FT TRANSMEM 418 438 POTENTIAL.
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 468 AA; 51781 MW; BF2C42D56ABB1B6D CRC64;

Query Match 55.2%; Score 32; DB 1; Length 468;
Best Local Similarity 87.5%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVVVPTM 8
Db 244 RTVVVPTM 251
|||| |||

RESULT 17
TRPE_ARATH STANDARD; PRT; 595 AA.
ID TRPE_ARATH
AC P32068;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Anthranilate synthase component I-1, chloroplast precursor
DE (EC 4.1.3.27).
GN ASAL OR AT5G05730 OR MJJ3.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005721; PubMed=1392592;
RA Miyogi K.K., Fink G.R.;
RT "Two anthranilate synthase genes in Arabidopsis: defense-related
RT regulation of the tryptophan pathway".
RL Plant Cell 4:721-733(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones".
RL DNA Res. 4:215-230(1997).
CC -!- CATALYTIC ACTIVITY: Chorismate + L-glutamine -> anthranilate +
CC pyruvate + L-glutamate.


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CC -1- PATHWAY: Tryptophan biosynthesis; first step.
CC -1- SUBUNIT: Tetramer of two components I and two components II.
CC -1- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
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CC -----
DR EMBL; M92353; AAA32738.1; -.
DR EMBL; AB005237; BAB09667.1; -.
DR EMBL; S27751; S27751.
DR HSP; Q06128; IQDL.
DR InterPro; IPR005256; Anth_synth1.
DR InterPro; IPR000350; Chorismate_bind.
DR Pfam; PF00445; Chorismate_bind; 1.
DR PRINTS; PR00095; ANTSNTHASE1.
DR PRODOM; PD000779; Chorismate_bind; 1.
DR TIGRFAMs; TIGR00564; trpE_most; 1.
DR Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide;
KW Multigene family.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 595 ANTHRANILATE SYNTHASE COMPONENT I-1.
SQ SEQUENCE 595 AA; 66311 MW; 674175416A2726F0 CRC64;

Query Match 55.28; Score 32; DB 1; Length 595;
Best Local Similarity 71.48; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVYPT 7
Db 526 RTIVPT 532
||:|:|

RESULT 18
NUSM_HYLLA STANDARD; PRT; 603 AA.
AC P03919;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN MTND5 OR ND5 OR NADH5.
OS Hylobates lar (Common gibbon).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Estes;
RA Arnason U., Gullberg A., Xu X.;
RT "A complete mitochondrial DNA molecule of the white-handed gibbon,
RT Hylobates lar, and comparison among individual mitochondrial genes of
RT all hominoid genera."
RN Hereditas 124:185-189(1996).
RL [2]
RP SEQUENCE OF 1-79 FROM N.A.
RX MEDLINE=62242101; PubMed=6284948;
RA Brown W.M., Prager E.M., Wang A., Wilson A.C.;
RT "Mitochondrial DNA sequences of primates: tempo and mode of
RT evolution."
RL J. Mol. Evol. 18:225-239(1982).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----

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CC -----
DR EMBL; X99256; CAA67638.1; -.
DR EMBL; V00659; CAA24025.1; -.
DR PIR; A00449; A00449.
DR InterPro; IPR003916; NADHub_Oxred5.
DR InterPro; IPR001750; Oxidored_q1.
DR InterPro; IPR001516; Oxidored_q1_N.
DR Pfam; PF00361; oxidored_q1; 1.
DR Pfam; PF00662; oxidored_q1_N; 1.
DR PRINTS; PR01434; NADHGNASE5.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 603 AA; 67360 MW; 3BFF99C6EA7BCE70 CRC64;

Query Match 55.28; Score 32; DB 1; Length 603;
Best Local Similarity 71.48; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VYPTMF 10
Db 48 LFTPTMF 54
::|:|:|

RESULT 19
RPOC_TREPA STANDARD; PRT; 1416 AA.
AC O83270;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR TP0242.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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KW EMBL: AE001205; AAC65230.1; -
DR HSPF; Q9RWU6; IHQM.
DR TIGR; TP0242; -
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 2.
KW Transferrase; DNA-directed RNA polymerase; Transcription;
KW Complete proteome.
SQ SEQUENCE 1416 AA; 159789 MW; 78D0EB6A1CA7C9C CRC64;

Query Match 55.2%; Score 32; DB 1; Length 1416;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVYPT 7 PRT; 1716 AA.
Db 486 RTVYPS 492
II:III:

RESULT 20
ID RPA1_RAT STANDARD; PRT; 1716 AA.
AC Q54889;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA
DE polymerase I 194 kDa subunit) (RPA194).
DE POLR1A OR RPA1-4 OR RPA1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086309; PubMed=9422795;
RA Hannan R.D., Hempel W.M., Cavanaugh A., Arino T., Dimitrov S.I.,
RA Moss T., Rothblum L.;
RT "Affinity purification of mammalian RNA polymerase I. Identification
RT of an associated kinase.";
RL J. Biol. Chem. 273:1257-1267(1998).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
CC RIBOSOMAL DNA UNITS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
CC DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS THE LARGEST COMPONENT OF
CC RNA POLYMERASE I.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND TRNA GENES.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
DR EMBL: AF025425; AB94601.1; -
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 2.
KW Transferrase; DNA-directed RNA polymerase; Transcription; Zinc;

KW Zinc-finger; Nuclear protein.
FT ZN_FING 64 80 C2H2-TYPE (POTENTIAL).
SQ SEQUENCE 1716 AA; 194191 MW; E8EE15BC23E60941 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 1716;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TVVYPTMFEK 11
Db 224 TITYPAVHK 233
II:III:

RESULT 21
ID RPOA_EAV STANDARD; PRT; 3175 AA.
AC P19811; Q88625;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE POL polyprotein (ORF1A/1B) [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
GN POL.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bucyrus;
RX MEDLINE=91237805; PubMed=1851863;
RA den Boon J.A., Sniijder E.J., Chirnside E.D., de Vries A.A.F.,
RA Horzinek M.C., Spaan W.J.M.;
RT "Equine arteritis virus is not a togavirus but belongs to the
RT coronaviruslike superfamily.";
RL J. Virol. 65:2910-2920(1991).
RN [2]
RP SEQUENCE OF 1-17 FROM N.A.
RC STRAIN=Bucyrus;
RX MEDLINE=90287699; PubMed=2162519;
RA de Vries A.A.F., Chirnside E.D., Bredenoek P.J., Gravestein L.A.,
RA Horzinek M.C., Spaan W.J.M.;
RT "All subgenomic mRNAs of equine arteritis virus contain a common
RT leader sequence.";
RL Nucleic Acids Res. 18:3241-3247(1990).
CC -!- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC ROLE FOR WTP-BINDING PROTEINS IN RNA DUPLEX UNWINDING HAS BEEN
CC SUGGESTED. ALSO CONTAINS A PROTEASE DOMAIN.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -!- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC FOR 1727-ASN AND 1728-LEU.
CC -!- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC OF TOROVIRUSES.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S32.
CC -----
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CC -----
DR EMBL: X53459; CAA37539.1; ALT-SEQ.
DR EMBL: X53459; CAA37540.1; ALT-SEQ.
DR EMBL: X52277; CAA36520.1; -
DR PIR; S10158; S10158.
DR MEROPS; C31.UNW; -
DR MEROPS; C32.001; -
DR MEROPS; C33.001; -
DR MEROPS; C33.001; -
DR MEROPS; S32.001; -

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DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1.
KW RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW Hydrolase; Serine protease; Zinc-finger.
FT CHAIN 1 1727 ORF1A.
FT CHAIN 1728 3175 ORF1B.
FT DOMAIN 1080 1220 TRYPSIN-LIKE SERINE PROTEASE.
FT DOMAIN 1218 1506 HELICASE.
FT DOMAIN 2098 2306 POLYMERASE.
FT ACT_SITE 1103 1103 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1129 1129 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1184 1184 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ZN_FING 2368 2414 BY SIMILARITY.
FT NP_BIND 2528 2535 ATP (BY SIMILARITY).
SQ SEQUENCE 3175 AA; 345275 MW; ED5C8BA0E31DE695 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 3175;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPTMFM 10
|:|:|:|
DB 1369 YPTMLF 1374

RESULT 22
SMPL_HUMAN STANDARD; PRT; 157 AA.
AC Q95807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small membrane protein 1.
GN SMPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu G.;
RT "A new member of the 18 kDa small membrane protein family in human.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RC MEDLINE=21154917; PubMed=11230166;
RX Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT VAL-58.
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO C21ORF4.
CC
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CC
CC EMBL; AF081282; AAD17754.1; -.
CC EMBL; AL136627; CAB66562.1; -.
CC
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DR EMBL; AF458851; AAL51108.1; -.
DR MIM; 605348; -.
KW Transmembrane; Polymorphism.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 95 115 POTENTIAL.
FT TRANSMEM 126 146 POTENTIAL.
FT VARIANT 58 58 A -> V.
FT VARIANT 141 141 F -> L.
FT SEQUENCE 157 AA; 17400 MW; 8CDF83AA23EBB1FA CRC64;

Query Match 53.4%; Score 31; DB 1; Length 157;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPTM 8
|:|:|:|
DB 44 VYPTM 49

RESULT 23
YQJL_ECOLI STANDARD; PRT; 207 AA.
ID YQJL_ECOLI
AC Q46872;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yqj1.
GN YQJ1 OR B3071.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna M.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
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CC
CC EMBL; U28379; AAA89150.1; -.
CC EMBL; AE000389; AAC76106.1; -.
CC EcoGene; EG12954; yqj1.
CC InterPro: IPR005149; PadR.
CC Pfam; PF03551; PadR; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 23401 MW; DD3D108D83E087F7 CRC64;

Query Match 53.4%; Score 31; DB 1; Length 207;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VYPTMFM 10
|:|:|:|
DB 99 VYPTLDF 106

RESULT 24
DNC_HUMAN
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ID DNC_HUMAN STANDARD; PRT; 320 AA.
AC Q9HC21;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
DE protein 1).
GN SLC25A19 OR DNC OR MUP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX PubMed=11226231;
RA Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.;
RT "The human mitochondrial deoxynucleotide carrier and its role in the
RT toxicity of nucleoside antivirals.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Renard S., Mondesert G., Besnard F.;
RT "MUP 1, a mitochondrial uncoupling protein.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Responsible for the uptake of deoxynucleotides into the
CC matrix of the mitochondria. Transports all four deoxy NDPs, and,
CC less efficiently, the corresponding dNTPs. Does not transport
CC dNTPs, NMPs, deoxynucleosides, nucleosides, purines, or
CC pyrimidines. Supply deoxynucleotides to the mitochondrial matrix
CC for conversion to triphosphates and incorporation into
CC mitochondrial DNA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined except for
CC placenta. Highest levels in colon, kidney, lung, testis, spleen,
CC and brain.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- DISEASE: Likely to be medically important by providing the means
CC of uptake into mitochondria of nucleoside analogs, leading to the
CC mitochondrial impairment that underlies the toxic side effects of
CC such drugs in the treatment of viral illnesses, including AIDS,
CC and in cancer therapy.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
DR EMBL; AJ251857; CAC27560.1; -
DR EMBL; AJ301616; CAC37793.1; -
DR EMBL; AF182404; ARG16903.1; -
DR EMBL; BC001075; AAH01075.1; -
DR EMBL; BC005120; AAH05120.1; -
DR EMBL; HGNC:14409; SLC25A19.
DR MIM; 606521; -
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 19 39 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.

FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 293 313 POTENTIAL.
SQ SEQUENCE 320 AA; 35511 MW; 57CE0F01D538B1BE CRC64;
Query Match 53.4%; Score 31; DB 1; Length 320;
Best Local Similarity 45.5%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 RTVVVPTMMFK 11
DB 231 KTLTYPLDLFK 241
RESULT 25
MSPL_YEAST STANDARD; PRT; 362 AA.
ID MSPL_YEAST
AC P28737;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MSPL protein (TAT-binding homolog 4).
GN MSPL OR YTA4 OR YGR028W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF747-19D;
RX MEDLINE=94043260; PubMed=8226973;
RA Nakai M., Endo T., Hase T., Matsubara H.;
RT "Intramitochondrial protein sorting. Isolation and characterization
RT of the yeast MSPL gene which belongs to a novel family of putative
RT ATPases.";
RL J. Biol. Chem. 268:24262-24269(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF747-19D;
RX MEDLINE=95274317; PubMed=7754704;
RA Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehmlé S.,
RT Schwarze C., Vetter I., Feldmann H.;
RT "Identification of a set of yeast genes coding for a novel family of
RT putative ATPases with high similarity to constituents of the 26S
RT protease complex.";
RL Yeast 10:1141-1155(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=97435481; PubMed=9290212;
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
RT chromosome VII.";
RL Yeast 13:1077-1090(1997).
RN [4]
RP SEQUENCE OF 280-362 FROM N.A.
RC STRAIN=SC167;
RX MEDLINE=92204135; PubMed=1552903;
RA Lisowsky T.;
RT "Dual function of a new nuclear gene for oxidative phosphorylation
RT and vegetative growth in yeast.";
RL Mol. Gen. Genet. 232:58-64(1992).
CC -1- FUNCTION: INVOLVED IN INTRAMITOCHONDRIAL SORTING OF PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC outer membrane.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X68055; CAA48191.1; -
DR EMBL; X81069; CAA56956.1; -
DR EMBL; Z72813; CAA97015.1; -
DR EMBL; X60722; -; NOT_ANNOTATED_CDS.
DR PIR; S20468; S20468.
DR PIR; S37410; S37410.
DR SGD; S0003260; MSP1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_Sub.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW ATP-binding; Mitochondrion; Outer membrane; Transmembrane.
FT DOMAIN 1 12 INTERMEMBRANE (POTENTIAL).
FT TRANSMEM 13 28 POTENTIAL.
FT DOMAIN 29 362 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 133 140 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 40343 MW; 1B3562A32F47F434 CRC64;

Query Match 53.4%; Score 31; DB 1; Length 362;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMM 9
Db :||| ||
106 SVIYPLMM 113
```

Search completed: July 16, 2003, 14:35:15
Job time : 27.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:45 ; Search time 41.6667 Seconds
(without alignments)
54.396 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	333	16 Q55184	Q55184 synechocyst
2	41	70.7	974	5 O01574	O01574 caenorhabdi
3	38	65.5	394	16 Q9CIU3	Q9ciw3 lactococcus
4	37	63.8	390	10 Q8VWX1	Q8vwx1 perilla fru
5	37	63.8	391	10 Q9ZPP7	Q9zpp7 perilla fru
6	37	63.8	395	16 Q9I2X4	Q9i2x4 pseudomonas
7	36	62.1	512	10 Q9LUC5	Q9luc5 arabidopsis
8	35	60.3	180	10 Q9FX69	Q9fx69 arabidopsis
9	35	60.3	254	10 Q93ZC5	Q93zc5 arabidopsis
10	35	60.3	258	10 Q9LS01	Q9ls01 arabidopsis
11	35	60.3	264	16 Q8ZLZ1	Q8z1z1 salmonella
12	35	60.3	282	10 Q94JV3	Q94jv3 arabidopsis
13	35	60.3	320	11 Q8VGS2	Q8vgs2 mus musculu
14	35	60.3	435	16 Q9WZ16	Q9wz16 thermotoga
15	35	60.3	504	12 Q9EME6	Q9eme6 ansacta moo
16	35	60.3	598	16 Q8Z3N6	Q8z3n6 salmonella

17	35	60.3	705	5 Q8SWA5	Q8swa5 encephalito
18	35	60.3	733	10 Q8S7E2	Q8s7e2 oryza sativ
19	35	60.3	735	10 Q9FJR9	Q9fjr9 arabidopsis
20	35	60.3	887	10 Q9ZVV2	Q9zvv2 arabidopsis
21	35	60.3	1030	3 Q9HFQ9	Q9hft9 emericeella
22	34	58.6	54	12 Q84121	Q84121 influenzavi
23	34	58.6	173	13 Q8U0Z6	Q8uuz6 brachydanio
24	34	58.6	180	16 Q98ID0	Q98id0 rhizobium l
25	34	58.6	212	16 Q8XNC4	Q8xnc4 clostridium
26	34	58.6	217	17 Q9HHU4	Q9hhu4 hloobacteri
27	34	58.6	303	10 Q64685	Q64685 arabidopsis
28	34	58.6	316	10 Q9LSV4	Q9lsv4 arabidopsis
29	34	58.6	320	17 Q8U223	Q8u223 pyrococcus
30	34	58.6	322	4 Q96LB2	Q96lb2 homo sapien
31	34	58.6	322	4 Q8TDD9	Q8td9 homo sapien
32	34	58.6	322	4 Q8TDD8	Q8td8 homo sapien
33	34	58.6	347	2 Q9KIS7	Q9kis7 brucella ab
34	34	58.6	347	16 Q8YDZ2	Q8ydz2 brucella me
35	34	58.6	373	2 Q95523	Q95523 photobacter
36	34	58.6	373	2 Q52100	Q52100 photobacter
37	34	58.6	389	16 Q8ZA85	Q8za85 versinia pe
38	34	58.6	404	16 Q8Z2F8	Q8z2f8 salmonella
39	34	58.6	464	10 Q9LEW3	Q9lew3 arabidopsis
40	34	58.6	530	17 Q97329	Q97329 sulfolobus
41	34	58.6	674	16 Q9WZS4	Q9wzs4 thermotoga
42	34	58.6	711	10 Q9C8R8	Q9c8r8 arabidopsis
43	33	57.8	1304	5 Q96959	Q96959 drosophila
44	33	57.8	1508	5 Q8T049	Q8t049 drosophila
45	33	57.8	1724	5 Q96960	Q96960 drosophila
46	33	57.8	1752	5 Q9U4K9	Q9u4k9 drosophila
47	33	57.8	1810	5 Q9V483	Q9v483 drosophila
48	33	56.9	120	16 Q31535	Q31535 bacillus su
49	33	56.9	159	8 Q950X8	Q950x8 tetrachyena
50	33	56.9	205	2 Q51516	Q51516 pseudomonas
51	33	56.9	205	16 Q9H0C4	Q9huc4 pseudomonas
52	33	56.9	221	16 Q8ZDB7	Q8zdb7 yersinia pe
53	33	56.9	237	10 Q8RX02	Q8rx02 arabidopsis
54	33	56.9	261	10 Q9SUW6	Q9suw6 arabidopsis
55	33	56.9	299	4 Q9NXA8	Q9nxa8 homo sapien
56	33	56.9	310	4 Q9Y6E6	Q9y6e6 homo sapien
57	33	56.9	390	16 Q8YFX4	Q8yfx4 brucella me
58	33	56.9	457	17 Q9HLH0	Q9hlh0 thermoplasma
59	33	56.9	457	17 Q978Q5	Q978q5 thermoplasma
60	33	56.9	474	10 Q43541	Q43541 lilium long
61	33	56.9	531	17 Q97V62	Q97v62 sulfolobus
62	33	56.9	703	12 Q83467	Q83467 porcine ade
63	33	56.9	725	5 Q9VD08	Q9vd08 drosophila
64	33	56.9	821	16 Q9RXG4	Q9rxg4 deinococcus
65	33	56.9	842	17 Q970B4	Q970b4 sulfolobus
66	33	56.9	1021	5 Q15733	Q15733 dictyostell
67	33	56.9	1063	4 Q8TDZ7	Q8tdz7 homo sapien
68	33	56.9	1235	16 Q929A9	Q929a9 listeria in
69	33	56.9	1235	16 Q8Y511	Q8y511 listeria mo
70	33	56.9	1824	5 Q9U0Y5	Q9u0y5 leishmania
71	32	55.2	61	10 Q8S6G8	Q8s6g8 oryza sativ
72	32	55.2	132	8 Q956K0	Q956k0 rhodotorula
73	32	55.2	136	16 Q8XFNO	Q8xfn0 salmonella
74	32	55.2	143	12 Q9WT48	Q9wt48 human herpe
75	32	55.2	143	12 Q9WYD9	Q9wdy9 human herpe

ALIGNMENTS

RESULT 1
Q55184
ID Q55184 PRELIMINARY; PRT; 333 AA.
AC Q55184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein sll0456.
GN SLL0456.

OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC 6803;
 RA Tabata S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RL "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RL "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D64001; BAA10324.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 333 AA; 37436 MW; 676E7399E4499ED6 CRC64;

Query Match 70.7%; Score 41; DB 16; Length 333;
 Best Local Similarity 77.8%; Pred. No. 6.5;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 |||||:
 172 TVVYPTLVF 180

RESULT 2
 O01574
 ID O01574 PRELIMINARY; PRT; 974 AA.
 AC O01574;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 111.6 kDa protein.
 GN F48C1.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RL "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Gattung S., Le T.T.;
 RL "The sequence of C. elegans cosmid F48C1.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;

"Direct Submission.";
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U97015; AAB52345.1;
 DR InterPro: IPR000602; Glyco_hydro_38.
 DR Pfam: PF01074; Glyco_hydro_38; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 974 AA; 111586 MW; C825EFA33FB2F964 CRC64;

Query Match 70.7%; Score 41; DB 5; Length 974;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
 :|::|||
 851 QTIYPPMMF 860

Db

RESULT 3
 Q9CIU3
 ID Q9CIU3 PRELIMINARY; PRT; 394 AA.
 AC Q9CIU3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ABC transporter ATP binding protein.
 GN YCGB OR LL0263.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarre K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RL "The complete genome sequence of the lactic acid bacterium Lactococcus
 lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 DR EMBL: AE006263; AAK04361.1;
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransportr.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 394 AA; 43946 MW; 2822CBG28AEA4C36 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 394;
 Best Local Similarity 66.7%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 |::|||
 47 TLIYPTMRF 55

Db

RESULT 4
 Q8VWX1
 ID Q8VWX1 PRELIMINARY; PRT; 390 AA.
 AC Q8VWX1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Delta-15 desaturase.
 GN FAD3.
 OS Perilla frutescens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.


```

OX NCBI_TaxID=48386;
RP SEQUENCE FROM N.A.
RN [1]
RC STRAIN=CV. OKONG; TISSUE=DEVELOPING SEED;
RA Kim K.-H., Hwang S.-K., Hwang Y.-S.;
RT "Cloning of Perilla delta-15 desaturase.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213482; AAL36934.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR ProDom: PD001081; FA_desaturase; 2.
SQ SEQUENCE 390 AA; 44857 MW; 6959C941D7A15AB CRC64;

Query Match 63.8%; Score 37; DB 10; Length 390;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
Db 1:111111
Db 241 TIVGPNMMFK 250

RESULT 5
Q9ZPP7 PRELIMINARY; PRT; 391 AA.
AC Q9ZPP7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Omega-3 fatty acid desaturase.
GN FAD3.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUWON-8;
RX MEDLINE=99205707; PubMed=10189709;
RA Chung C.-H., Kim J.-L., Lee Y.-C., Choi Y.-L.;
RT "Cloning and characterization of a seed-specific omega-3 fatty acid
desaturase cDNA from Perilla frutescens.";
RL Plant Cell Physiol. 40:114-118(1999).
DR EMBL; AF047039; AAD15744.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR ProDom: PD001081; FA_desaturase; 2.
SQ SEQUENCE 391 AA; 44931 MW; 6637E81654C17CEC CRC64;

Query Match 63.8%; Score 37; DB 10; Length 391;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
Db 1:111111
Db 242 TIVGPNMMFK 251

RESULT 6
Q912X4 PRELIMINARY; PRT; 395 AA.
AC Q912X4;
DT 01-MAY-2001 (TREMBlrel. 16, Created)
DT 01-MAY-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical protein PA1765.
GN PA1765.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004602; AAG05154.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 395 AA; 44670 MW; FC183A433B2529C8 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 395;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
Db 1:111111
Db 292 ROVYPSLLF 301

RESULT 7
Q9LUC5 PRELIMINARY; PRT; 512 AA.
AC Q9LUC5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome P450 (Putative cytochrome P450 protein).
GN MIE1.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty p1 and TAC
clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Ouach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MIE1.20 (GI:9294391).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AB023038; BAB02401.1; -.
DR EMBL; AY050827; AAK92762.1; -.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; p450; 1.
DR PRINTS; PR00385; P450.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 512 AA; 58442 MW; 19DDEAD9C9BAF0B CRC64;

```

Query Match 62.18; Score 36; DB 10; Length 512;
Best Local Similarity 63.6%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 11
| | | | |
DB 80 RVVPYPLQMK 90

RESULT 8

Q9FX69 Q9FX69 PRELIMINARY; PRT; 180 AA.
AC Q9FX69;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE T674.4 protein.
GN T674.4.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao O., Chin C., Chiou J., Choi E., Gonzalez A.,
RA Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AC011810; AAG09557.1; -.
DR EMBL: 180 AA; 1979 MW; 5DA0943DB333F332 CRC64;
SQ SEQUENCE 180 AA; 1979 MW; 5DA0943DB333F332 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 180;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 10
| | | | |
DB 124 RQLVYPTKLF 133

RESULT 9

Q93ZC5 Q93ZC5 PRELIMINARY; PRT; 254 AA.
AC Q93ZC5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE At1g13280/T674.23.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
OS Arabidopsis cDNA clones.*;
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY057636; AAL15267.1; -.
DR EMBL: 254 AA; 27809 MW; 4D82FA4889242353 CRC64;
SQ SEQUENCE 254 AA; 27809 MW; 4D82FA4889242353 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 254;
Best Local Similarity 60.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 10
| | | | |
DB 198 RQLVYPTKLF 207

RESULT 10

Q9LS01 Q9LS01 PRELIMINARY; PRT; 258 AA.
AC Q9LS01;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Genomic DNA, chromosome 3, TAC clone:K13N2.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.,
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=108193329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty pl and TAC clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL: AB028607; BAA95765.1; -.
SQ SEQUENCE 258 AA; 28398 MW; 42AF942E0E9AAB87 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 258;
Best Local Similarity 60.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 10
| | | | |
DB 202 RQLVYPTKLF 211

RESULT 11

Q8ZLZ1 Q8ZLZ1 PRELIMINARY; PRT; 264 AA.
AC Q8ZLZ1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative arylsulfate sulfotransferase.
GN STM3192.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";


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RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094;
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT Analysis and Comparison with Other Poxviruses.";
RL Virology 274:120-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250284; AAG02966.1; -.
SQ SEQUENCE 504 AA; 61862 MW; ACA9BFFA559FAA50 CRC64;

Query Match 60.3%; Score 35; DB 12; Length 504;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TVVYPTMMFK 11
Db 459 TVIPSLLLR 468

RESULT 16
Q8Z3N6
ID Q8Z3N6 PRELIMINARY; PRT; 598 AA.
AC Q8Z3N6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable arylsulfate sulfotransferase.
GN SY3370.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627278; CAB07717.1; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 598 AA; 66586 MW; B5434F028A5421F0 CRC64;

Query Match 60.3%; Score 35; DB 16; Length 598;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMFK 11
Db 590 LVHPTQMK 598

RESULT 17
Q8SWA5
ID Q8SWA5 PRELIMINARY; PRT; 705 AA.
AC Q8SWA5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein ECU02_1230.

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GN ECU02_1230.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590442; CAD25152.1; -.
KW Hypothetical protein.
SQ SEQUENCE 705 AA; 79649 MW; 235B8334A40258AEF CRC64;

Query Match 60.3%; Score 35; DB 5; Length 705;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TVVYPTMM 9
Db 570 TVIYPTLL 577

RESULT 18
Q8S7E2
ID Q8S7E2 PRELIMINARY; PRT; 733 AA.
AC Q8S7E2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 82.3 kDa protein.
GN OSJNBA0057L21.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pal G.,
RA VanAken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA0057L21 genomic sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC087599; AAL79699.1; -.
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82297 MW; 24C8521E18220D9D CRC64;

Query Match 60.3%; Score 35; DB 10; Length 733;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
Db 462 RRVVYPTLRY 471

RESULT 19
Q9FJR9
ID Q9FJR9 PRELIMINARY; PRT; 735 AA.

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Query Match 58.6%; Score 34; DB 12; Length 54;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVVYPTM 8
Db 43 QTVVYPTI 50
:|||||:

RESULT 23

Q8UUZ6 PRELIMINARY; PRT; 173 AA.
ID Q8UUZ6
AC Q8UUZ6
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Alpha A crystallin.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
ON NCBI_TaxID=7955;
RN [1]
RC SEQUENCE FROM N.A.
PC TISSUE=LENS;
RA Runkle S., Hill J., Kantorow M., Horwitz J., Posner M.;
RT "Cloning and characterization of zebrafish (Danio rerio) alpha A-crystallin";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY035778; AAK61363.1; -
DR InterPro: IPR001436; Crystallin_alpha.
DR InterPro: IPR003090; Crystallin_N.
DR InterPro: IPR002068; Hsp20.
DR Pfam: PF00525; Crystallin; 1.
DR Pfam: PF00011; HSP20; 1.
DR PRINTS: PR00299; ACRYSTALLIN.
DR PRODOM: PD001193; Crystallin_N; 1.
DR PROSITE: PS01031; HSP20; 1.
SQ SEQUENCE 173 AA; 19714 MW; 301D743DB91BBC13 CRC64;

Query Match 58.6%; Score 34; DB 13; Length 173;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMFM 10
Db 12 RTLGYPTRLF 21
||: |||:

RESULT 24

Q98ID0 PRELIMINARY; PRT; 180 AA.
ID Q98ID0
AC Q98ID0
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein ml12459.
GN MLL2459.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
ON NCBI_TaxID=381;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti.;
RL DNA Res. 7:331-338(2000).
DR EMBL: AP002999; BAB49586.1; -
DR InterPro: IPR005149; PdrR.
DR Pfam: PF03551; PdrR; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 180 AA; 19909 MW; D94F736B2855CF60 CRC64;

Query Match 58.6%; Score 34; DB 16; Length 180;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMF 10
Db 49 VVYPTLTF 56
|||||:

RESULT 25

Q8XNC4 PRELIMINARY; PRT; 212 AA.
ID Q8XNC4
AC Q8XNC4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein CPE0414.
GN CPE0414.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
ON NCBI_TaxID=1502;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AP003186; BAB80120.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 212 AA; 24363 MW; DB7E1E2AC94BE697 CRC64;

Query Match 58.6%; Score 34; DB 16; Length 212;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VVYPTMMFK 11
Db 205 IYPNMIFK 212
:|||:|:

Search completed: July 16, 2003, 14:37:07
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 44.3333 Seconds
(without alignments)
33.062 Million cell updates/sec

Title: US-09-923-716c-4
Perfect score: 58
Sequence: 1 RTVVYPTMFX 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	65.5	207	AA29277	Arabidopsis thalia
2	38	65.5	262	AA27262	Plant steroid 5-al
3	38	65.5	262	AA29276	Arabidopsis thalia
4	38	65.5	394	ABBS3569	Lactococcus lactis
5	37	63.8	560	ABG29423	Novel human diago
6	36	62.1	82	AAO10186	Human polypeptide
7	35	60.3	242	AAO9307	Arabidopsis thalia
8	35	60.3	244	AAO9361	Arabidopsis thalia
9	35	60.3	244	AA29277	Arabidopsis thalia
10	35	60.3	246	AA29277	Soybean neutral tr

11	35	60.3	251	21	AA29277	Arabidopsis thalia
12	35	60.3	251	21	AA29277	Arabidopsis thalia
13	35	60.3	252	21	AA29277	Arabidopsis thalia
14	35	60.3	254	21	AA29277	Arabidopsis thalia
15	35	60.3	254	22	AA29277	A. thaliana allene
16	35	60.3	254	23	AA29277	Herbicidally activ
17	35	60.3	258	21	AA29277	Arabidopsis thalia
18	35	60.3	258	21	AA29277	Arabidopsis thalia
19	34	58.6	56	21	AA29277	Arabidopsis thalia
20	34	58.6	56	21	AA29277	Arabidopsis thalia
21	34	58.6	57	21	AA29277	Arabidopsis thalia
22	34	58.6	57	21	AA29277	Arabidopsis thalia
23	34	58.6	264	21	AA29277	Arabidopsis thalia
24	34	58.6	264	21	AA29277	Arabidopsis thalia
25	34	58.6	264	22	AA29277	Human protein SEQ
26	34	58.6	266	21	AA29277	Arabidopsis thalia
27	34	58.6	267	21	AA29277	Arabidopsis thalia
28	34	58.6	322	20	AA29277	Human dorsal root
29	34	58.6	322	20	AA29277	Human dorsal root
30	34	58.6	322	22	AA29277	Human G protein co
31	34	58.6	322	22	AA29277	Human G-protein co
32	34	58.6	322	22	AA29277	Human Gp-binding
33	34	58.6	322	23	AA29277	Human MrpX1 (mas-r
34	34	58.6	322	23	AA29277	Human G-protein co
35	34	58.6	591	21	AA29277	Rhinocladella atr
36	34	58.6	598	21	AA29277	Rhinocladella atr
37	33.5	57.8	1810	22	AA29277	Drosophila melanog
38	33	56.9	99	23	AA29277	Human ovarian anti
39	33	56.9	310	21	AA29277	Human nucleic acid
40	33	56.9	593	22	AA29277	Propionibacterium
41	33	56.9	609	20	AA29277	Adenovirus PACTSSI
42	33	56.9	609	20	AA29277	Adenovirus P1g4KN
43	33	56.9	656	22	AA29277	C glutamicum prote
44	33	56.9	700	22	AA29277	Yeast RFI. Uniden
45	33	56.9	725	22	AA29277	Drosophila melanog
46	33	56.9	750	20	AA29277	Adenovirus PNPSP194
47	33	56.9	1235	23	AA29277	Listeria monocytog
48	32	55.2	66	22	AA29277	Propionibacterium
49	32	55.2	72	23	AA29277	Human ORP2716 prot
50	32	55.2	74	23	AA29277	Human immune/haema
51	32	55.2	93	22	AA29277	Propionibacterium
52	32	55.2	137	22	AA29277	Propionibacterium
53	32	55.2	156	22	AA29277	Propionibacterium
54	32	55.2	283	23	AA29277	Listeria monocytog
55	32	55.2	358	23	AA29277	Hydratase-aldorase
56	32	55.2	446	20	AA29277	Corn anthranilate
57	32	55.2	447	22	AA29277	Streptococcus pyog
58	32	55.2	447	22	AA29277	Streptococcus pyog
59	32	55.2	447	23	AA29277	Streptococcus poly
60	32	55.2	462	21	AA29277	Amino polyol amine
61	32	55.2	462	21	AA29277	Amino polyol amine
62	32	55.2	462	21	AA29277	Amino acid sequenc
63	32	55.2	462	21	AA29277	Amino acid sequenc
64	32	55.2	463	21	AA29277	Amino polyol amine
65	32	55.2	463	21	AA29277	Amino acid sequenc
66	32	55.2	487	21	AA29277	Amino polyol amine
67	32	55.2	487	21	AA29277	An aminopolylol ami
68	32	55.2	491	20	AA29277	Tobacco anthranila
69	32	55.2	519	23	AA29277	Streptococcus poly
70	32	55.2	526	23	AA29277	Herbicidally activ
71	32	55.2	554	21	AA29277	Amino polyol amine
72	32	55.2	554	21	AA29277	An aminopolylol ami
73	32	55.2	577	20	AA29277	Rice ASA first iso
74	32	55.2	577	20	AA29277	Rice anthranilate
75	32	55.2	595	23	AA29277	Herbicidally activ

ALIGNMENTS

RESULT 1
AAG29277
ID AAG29277 standard; Protein; 207 AA.

XX AC AAG29277; 99US-0139462.
XX AC 17-OCT-2000 (first entry) 99US-0139463.
XX DT 18-JUN-1999; 99US-0139750.
XX XX 18-JUN-1999; 99US-0139763.
XX DE 21-JUN-1999; 99US-0139817.
XX XX 22-JUN-1999; 99US-0139899.
XX KW Protein identification; signal transduction pathway; metabolic pathway; 99US-0140353.
KW hybridisation assay; genetic mapping; gene expression control; promoter; 99US-0140354.
KW termination sequence. 99US-0140695.
XX OS 28-JUN-1999; 99US-0140823.
XX OS Arabidopsis thaliana. 99US-0140991.
XX PN EP1033405-A2. 99US-0141287.
XX XX 01-JUL-1999; 99US-0141842.
XX XX 01-JUL-1999; 99US-0142154.
XX PD 02-JUL-1999; 99US-0142055.
XX XX 06-JUL-1999; 99US-0142390.
XX XX 08-JUL-1999; 99US-0142803.
XX XX 09-JUL-1999; 99US-0142920.
XX XX 12-JUL-1999; 99US-0142977.
XX XX 13-JUL-1999; 99US-0143542.
XX XX 14-JUL-1999; 99US-0143624.
XX XX 15-JUL-1999; 99US-0144005.
XX XX 16-JUL-1999; 99US-0144085.
XX XX 16-JUL-1999; 99US-0144086.
XX XX 19-JUL-1999; 99US-0144325.
XX XX 19-JUL-1999; 99US-0144331.
XX XX 19-JUL-1999; 99US-0144332.
XX XX 19-JUL-1999; 99US-0144333.
XX XX 19-JUL-1999; 99US-0144334.
XX XX 19-JUL-1999; 99US-0144335.
XX XX 20-JUL-1999; 99US-0144352.
XX XX 20-JUL-1999; 99US-0144632.
XX XX 20-JUL-1999; 99US-0144884.
XX XX 21-JUL-1999; 99US-0144814.
XX XX 21-JUL-1999; 99US-0145086.
XX XX 21-JUL-1999; 99US-0145088.
XX XX 22-JUL-1999; 99US-0145085.
XX XX 22-JUL-1999; 99US-0145087.
XX XX 22-JUL-1999; 99US-0145089.
XX XX 22-JUL-1999; 99US-0145192.
XX XX 23-JUL-1999; 99US-0145145.
XX XX 23-JUL-1999; 99US-0145218.
XX XX 23-JUL-1999; 99US-0145224.
XX XX 26-JUL-1999; 99US-0145276.
XX XX 27-JUL-1999; 99US-0145913.
XX XX 27-JUL-1999; 99US-0145918.
XX XX 27-JUL-1999; 99US-0145919.
XX XX 28-JUL-1999; 99US-0145951.
XX XX 02-AUG-1999; 99US-0146386.
XX XX 02-AUG-1999; 99US-0146389.
XX XX 02-AUG-1999; 99US-0146388.
XX XX 03-AUG-1999; 99US-0147038.
XX XX 04-AUG-1999; 99US-0147204.
XX XX 04-AUG-1999; 99US-0147302.
XX XX 05-AUG-1999; 99US-0147192.
XX XX 05-AUG-1999; 99US-0147260.
XX XX 06-AUG-1999; 99US-0147303.
XX XX 06-AUG-1999; 99US-0147416.
XX XX 09-AUG-1999; 99US-0147493.
XX XX 09-AUG-1999; 99US-0147935.
XX XX 10-AUG-1999; 99US-0148171.
XX XX 11-AUG-1999; 99US-0148319.
XX XX 12-AUG-1999; 99US-0148341.
XX XX 13-AUG-1999; 99US-0148565.
XX XX 13-AUG-1999; 99US-0148684.
XX XX 16-AUG-1999; 99US-0149368.
XX XX 17-AUG-1999; 99US-0149175.
XX XX 18-AUG-1999; 99US-0149426.
XX XX 20-AUG-1999; 99US-0149722.
XX XX 20-AUG-1999; 99US-0149723.
XX XX 20-AUG-1999; 99US-0149929.
XX XX 23-AUG-1999; 99US-0149902.
XX XX 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.5%; Score 38; DB 21; Length 207;
 Best Local Similarity 45.5%; Pred. No. 9.2;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 11
 ||::|| :|:
 Db 38 RTIYPLRLFR 48

RESULT 2

AAW27262

ID AAW27262 standard; Protein; 262 AA.

XX AC

AAW27262;

XX XX

DT 23-APR-1998 (first entry)

XX XX

DE Plant steroid 5-alpha reductase DET2.

XX XX

KW Plant steroid 5-alpha reductase; Arabidopsis; DET2; pest resistance;
 KW brassinolide biosynthesis; growth.
 XX Arabidopsis sp.
 OS Arabidopsis sp.
 PN WO9739112-A1.
 XX 23-OCT-1997.
 PD 23-OCT-1997.
 XX 14-APR-1997; 97WO-US061115.
 XX 18-APR-1996; 96US-0634475.
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA Chory J, Li J;
 PI WPI; 1997-526449/48.
 XX N-PSDB; AAT91260.
 DR New isolated plant steroid 5-alpha reductase gene, DET2 - used to
 PT develop products for e.g. increasing plant yield and pest resistance
 PT or for producing plants with reduced stature
 PS Claim 4; Page 45-46; 70pp; English.
 XX The present sequence represents a novel plant steroid 5-alpha reductase,
 CC DET2. Methods have also been developed for producing plants with
 CC increased yield, as compared to wild-type. The DET2 polypeptides have
 CC 5AR activity and are involved in the brassinolide biosynthesis pathway.
 CC The products and methods can be used to produce modified plants which
 CC can exhibit increased plant growth, increased crop yield or increased
 CC biomass. The plants can also have increased resistance to pests and
 CC pesticides. Inhibitors of DET2 can be used to cause loss of function of
 CC DET2 resulting in, e.g. male sterile plants or reduced stature (dwarf
 CC plants).
 XX SQ Sequence 262 AA;
 Query Match 65.5%; Score 38; DB 18; Length 262;
 Best Local Similarity 45.5%; Pred. No. 12;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RTVVYPTMFK 11
 ||::|| :|:
 Db 93 RTIYPLRLFR 103
 RESULT 3
 AAG29276
 ID AAG29276 standard; Protein; 262 AA.
 XX AC
 XX AAG29276;
 XX XX
 XX 17-OCT-2000 (first entry)
 DT XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 34805.
 XX XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 PN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-0301439.
 PF 25-FEB-1999; 99US-0121825.
 XX 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR

PR	23-MAR-1999;	99US-0125788.	PR	16-JUL-1999;	99US-0144085.
PR	25-MAR-1999;	99US-0126264.	PR	18-JUL-1999;	99US-0144086.
PR	29-MAR-1999;	99US-0126785.	PR	19-JUL-1999;	99US-0144325.
PR	01-APR-1999;	99US-0127462.	PR	19-JUL-1999;	99US-0144331.
PR	06-APR-1999;	99US-0128234.	PR	19-JUL-1999;	99US-0144332.
PR	08-APR-1999;	99US-0128714.	PR	19-JUL-1999;	99US-0144333.
PR	16-APR-1999;	99US-0129845.	PR	19-JUL-1999;	99US-0144334.
PR	19-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR	21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR	23-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144632.
PR	23-APR-1999;	99US-0130891.	PR	20-JUL-1999;	99US-0144884.
PR	28-APR-1999;	99US-0131149.	PR	21-JUL-1999;	99US-0144814.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
PR	30-APR-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR	04-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145085.
PR	05-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145089.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145192.
PR	07-MAY-1999;	99US-0132487.	PR	23-JUL-1999;	99US-0145145.
PR	11-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145218.
PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134218.	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	99US-0134219.	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	99US-0134221.	PR	27-JUL-1999;	99US-0145918.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145919.
PR	18-MAY-1999;	99US-0134768.	PR	28-JUL-1999;	99US-0145951.
PR	18-MAY-1999;	99US-0134768.	PR	02-AUG-1999;	99US-0146386.
PR	19-MAY-1999;	99US-0134941.	PR	02-AUG-1999;	99US-0146388.
PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0146389.
PR	21-MAY-1999;	99US-0135353.	PR	03-AUG-1999;	99US-0147038.
PR	24-MAY-1999;	99US-0135629.	PR	04-AUG-1999;	99US-0147204.
PR	25-MAY-1999;	99US-0136021.	PR	04-AUG-1999;	99US-0147302.
PR	27-MAY-1999;	99US-0136392.	PR	05-AUG-1999;	99US-0147192.
PR	28-MAY-1999;	99US-0136782.	PR	05-AUG-1999;	99US-0147260.
PR	01-JUN-1999;	99US-0137222.	PR	06-AUG-1999;	99US-0147303.
PR	03-JUN-1999;	99US-0137528.	PR	06-AUG-1999;	99US-0147416.
PR	04-JUN-1999;	99US-0137502.	PR	09-AUG-1999;	99US-0147493.
PR	07-JUN-1999;	99US-0137724.	PR	09-AUG-1999;	99US-0147935.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0148171.
PR	10-JUN-1999;	99US-0138540.	PR	11-AUG-1999;	99US-0148319.
PR	10-JUN-1999;	99US-0138847.	PR	12-AUG-1999;	99US-0148341.
PR	14-JUN-1999;	99US-0139119.	PR	13-AUG-1999;	99US-0148565.
PR	16-JUN-1999;	99US-0139452.	PR	13-AUG-1999;	99US-0148684.
PR	16-JUN-1999;	99US-0139453.	PR	16-AUG-1999;	99US-0149368.
PR	17-JUN-1999;	99US-0139492.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139454.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139455.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139456.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139459.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139461.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139462.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139463.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151066.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	30-AUG-1999;	99US-0151080.
PR	21-JUN-1999;	99US-0139899.	PR	31-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	01-SEP-1999;	99US-0151930.
PR	23-JUN-1999;	99US-0140354.	PR	07-SEP-1999;	99US-0152363.
PR	24-JUN-1999;	99US-0140695.	PR	10-SEP-1999;	99US-0153070.
PR	28-JUN-1999;	99US-0140823.	PR	13-SEP-1999;	99US-0153758.
PR	29-JUN-1999;	99US-0140991.	PR	15-SEP-1999;	99US-0154018.
PR	30-JUN-1999;	99US-014287.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0141842.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142154.	PR	22-SEP-1999;	99US-0155139.
PR	02-JUL-1999;	99US-0142055.	PR	23-SEP-1999;	99US-0155486.
PR	06-JUL-1999;	99US-0142390.	PR	24-SEP-1999;	99US-0155659.
PR	08-JUL-1999;	99US-0142803.	PR	28-SEP-1999;	99US-0156458.
PR	09-JUL-1999;	99US-0142920.	PR	29-SEP-1999;	99US-0156596.
PR	12-JUL-1999;	99US-0142977.	PR	04-OCT-1999;	99US-0157117.
PR	13-JUL-1999;	99US-0143542.	PR	05-OCT-1999;	99US-0157753.
PR	14-JUL-1999;	99US-0143624.	PR	06-OCT-1999;	99US-0157865.
PR	15-JUL-1999;	99US-0144005.			

PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.5%; Score 38; DB 21; Length 262;

Best Local Similarity 45.5%; Pred. No. 12;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RTVYPTMMFK 11
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 Db 93 RTIYPLRLFR 103

RESULT 4

ID ABB53569 standard; Protein; 394 AA.

AC ABB53569;

DT 16-MAY-2002 (first entry)

DE Lactococcus lactis protein ycgB.

KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

OS Lactococcus lactis IL1403.

PN FR2807446-A1.

PD 12-OCT-2001.

XX 11-APR-2000; 2000FR-0004630.

XX 11-APR-2000; 2000FR-0004630.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX WPI; 2002-043418/06.

XX New nucleotide sequence useful in the identification or Lactococcus
 PT lactic acid and related species -

XX Claim 6; SEQ ID No 271; 2504pp; French.

XX

CC The present invention is related to a Lactococcus lactis nucleotide
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
 CC nucleic acid sequence is useful in the detection and/or amplification of
 CC nucleic acid sequence, particularly to identify Lactococcus lactis or
 CC related species. The proteins of the invention are useful for the
 CC biosynthesis or biodegradation of a composition of interest. The
 CC invention helps research in lactic bacteria, particularly useful in the
 CC production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent
 CC WO200177334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 394 AA;

Query Match 65.5%; Score 38; DB 23; Length 394;

Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TVVYPTMMF 10

Db 47 TLIYPTMRF 55

RESULT 5

ABG29423

ID ABG29423 standard; Protein; 560 AA.

AC ABG29423;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #29414.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS93610.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 20; SEQ ID No 59782; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 560 AA;

Query Match 63.8%; Score 37; DB 22; Length 560;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVPTMMF 10
Db 214 TLVIPTMMF 222
I:| |||||

RESULT 6
AAO10186
ID AAO10186 standard; Protein; 82 AA.

AC AAO10186;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 24078.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI90117.

PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -

XX Claim 20; SEQ ID NO 24078; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 82 AA;

Query Match 62.1%; Score 36; DB 22; Length 82;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPTMMFK 11
Db 1 YPTMIFK 7
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AAG09307

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XX 17-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

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Best Local Similarity

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60.0%; Pred. No. 45;

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XX 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS EPI033405-A2.
PN 06-SEP-2000.
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QY 1 RTVVYPTMMF 10
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 Db 188 ROLVYPTKLF 197

RESULT 10
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 ID AAY32315 standard; Protein; 246 AA.
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 AC AAY32315;
 XX
 DT 28-FEB-2000 (first entry)

XX DE Soybean neutral triacylglycerol lipase.
 XX KW Triacylglycerol lipase; soybean; fatty acid; seed oil;
 XX KW vegetable oil; transgenic plant.
 XX OS Glycine max.
 XX OS W09955883-A2.
 XX PN 04-NOV-1999.
 XX PD
 XX PF
 XX PR 25-FEB-1999; 99US-0121825.
 XX PR 05-MAR-1999; 99US-0123180.
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KW termination sequence.
 XX Arabidopsis thaliana.
 XX EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PF 25-FEB-2000; 2000EP-0301439.
 XX PR 25-FEB-1999; 99US-0121825.
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Query Match 60.3%; Score 35; DB 21; Length 246;
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 Db 75 ILVPTMFM 82

RESULT 11
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 ID AAG07360 standard; Protein; 251 AA.
 XX
 AC AAG07360;
 XX
 XX 17-OCT-2000 (first entry)
 DT
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 4484.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW

Novel plant triacylglycerol lipase polynucleotides used to alter the level of the enzyme in transgenic plants -
 Claim 10; Page 58-59; 65pp; English.
 This sequence represents most of a soybean neutral triacylglycerol lipase (TAGL), as deduced from the nucleotide sequence of isolated cDNA clones (see AAZ34964). Novel acid and neutral TAGL polypeptides (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn, Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes may be prepared recombinantly and used to raise antibodies, which are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacylglycerol and cholesterol esters found in those cells. Accumulation of fatty acids with unusual structures may be a positive phenotype in plants used for foods. In addition, it may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the design and/or identification of inhibitors of those enzymes that may be useful as herbicides. This is desirable because inhibition of the activity of either of the enzymes could lead to an inhibition of plant growth.

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Query Match 60.3%; Score 35; DB 21; Length 251;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12
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XX
AC AAG61262;

DT 18-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 79442.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

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PR 01-SEP-1999; 99US-0151930.
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PR 07-OCT-1999; 99US-0158029.
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Query Match 60.3%; Score 35; DB 21; Length 254;
 Best Local Similarity 60.0%; Pred. No. 47;
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QY 1 RTVYPTMMF 10
 Db 198 RQLVPTKLF 207

RESULT 15
 AAB86353
 ID AAB86353 standard; Protein; 254 AA.

XX AAB86353;

DT 20-SEP-2001 (first entry)

DE A. thaliana allene oxide cyclase protein SEQ ID 10.

XX Allene oxide cyclase; jasmonic acid; plant; AOC; jasmonate biosynthesis;
 KW signalling molecule; gene expression; stress response; perfume synthesis;
 KW wound-induced signal cascade; defensive response; transgenic plant;
 KW protease inhibitor synthesis; phytoalexin synthesis; alkaloid synthesis;
 KW pathogen resistance; herbicide resistance; ultra-violet protection;
 KW secondary metabolite production; male sterility; flower development;
 KW seed formation; germination.

XX Arabidopsis thaliana.

OS WO200157224-A2.

PN 09-AUG-2001.

PD 02-FEB-2001; 2001WO-EP01148.

PF 02-FEB-2000; 2000DE-1004468.

XX (PFLA-) INST PFLANZENBIOCHEMIE.

XX Ziegler J, Stenzel I, Hause B, Wasternack C;

PI WPI; 2001-483438/52.

XX N-PSDB; AAR21490.

PT Nucleic acid encoding plant allene oxide cyclase, useful for producing
 PT transgenic plants with altered jasmonic acid synthesis, e.g. increased
 PT resistance to pathogens -

XX Claim 1b; Page 55-56; 66pp; German.

XX

CC This invention describes novel nucleic acids (I), encoding proteins
 CC (II) with the activity of the allene oxide cyclase (AOC) involved in
 CC jasmonate biosynthesis. Jasmonic acid (JA) is a signalling molecule
 CC involved in: (i) altered gene expression in plants in response to
 CC stress; and (ii) developmental processes. It is also an intermediate in
 CC the wound-induced signal cascade and induces many defensive responses in
 CC plants, including synthesis of protease inhibitors, phytoalexins,
 CC alkaloids and perfumes. (I) is used: (i) to produce transgenic plants,
 CC cells etc. with altered AOC activity, specifically altered resistance to
 CC pathogens and herbivores, optimal plant/useful insect/pest interaction;
 CC increased biomass, altered carbohydrate and nitrogen metabolism;
 CC increased production of secondary metabolites (especially alkaloids
 CC and/or phytoalexins), optimal ultra-violet protection; altered male
 CC sterility and/or altered development, especially flower development, seed
 CC formation and/or germination; (ii) for selective production of 9S/13S
 CC (cis(+))-12-oxophytodienoic acid (III), a precursor of jasmonic acid
 CC (JA); (iii) for isolation of homologous sequences; and (iv) to express
 CC AOC in prokaryotic or eukaryotic cells or (in antisense orientation) to
 CC inhibit its expression. (I) Makes possible large scale production of high
 CC purity JA. (I) is very specific for production of (III) (contrast
 CC non-enzymatic methods which produce mixtures of isomers) which is a
 CC precursor for the natural enantiomer of JA. This sequence represents the
 CC Arabidopsis thaliana AOC described in the invention.

XX Sequence 254 AA;

Query Match 60.3%; Score 35; DB 22; Length 254;

Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10

Db 198 RQLVPTKLF 207

RESULT 16

AAB90980

ID AAB90980 standard; Protein; 254 AA.

XX AAB90980;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 191.

XX Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP09892.

PR 28-AUG-2001; 2001WO-EP09892.

PA (FARB) BAYER AG.

XX Tietjen K, Weidner M;

XX WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms -

XX Claim 5; SEQ ID NO 191; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins

CC (AAB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant
 CC with nucleic acid or amino acid sequences from non-plant organisms using
 CC suitable search parameters, where plant sequences having an E-value
 CC greater by a factor of 3 than the E-value of most similar non-plant
 CC sequences are selected. The polypeptides or nucleic acids encoding them
 CC are useful for identifying modulators. The identified modulators are
 CC useful as herbicides.

XX Sequence 254 AA;

Query Match 60.3%; Score 35; DB 23; Length 254;

Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMMF 10

Db 198 RQLVPTKLF 207

RESULT 17

AAG07359

ID AAG07359 standard; Protein; 258 AA.

XX AC

XX AC

XX DT

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 4483.

DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

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XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

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 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
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PR 29-OCT-1999; 99US-0162142.

Query Match      60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db      202 RQLVYPTKLF 211

RESULT 18
AAG61261
ID AAG61261 standard; Protein; 258 AA.
XX
AC AAG61261;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79441.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
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Db      202 ROLVPTKLF 211

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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 45.5%; Pred. No. 14;
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Db 28 KLIVPTROYK 38

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AC XX AAG60760;
DT XX 18-OCT-2000 (first entry)
XX XX Arabidopsis thaliana protein fragment SEQ ID NO: 78740.
DE XX Protein identification; signal transduction pathway; metabolic pathway;
KW KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW KW termination sequence.
XX XX Arabidopsis thaliana.
XX XX EP1033405-A2.
PD XX 06-SEP-2000.
XX XX 25-FEB-2000; 2000EP-0301439.
XX XX 25-FEB-1999; 99US-0121825.
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Query Match 58.6%; Score 34; DB 21; Length 56;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
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AC AAG55170;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70700.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
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Query Match 58.6%; Score 34; DB 21; Length 57;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 29 KLIVPTQYK 39

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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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Query Match 58.6%; Score 34; DB 21; Length 57;
Best Local Similarity 45.5%; Pred. No. 14;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 29 KLIVPTROYK 39
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RESULT 23

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XX AC AAG05880;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 2450.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

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Query Match 58.6%; Score 34; DB 21; Length 264;
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KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US04098.
XX PP 03-FEB-2000; 2000US-0496914.
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PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI: 2001-476283/51.
 DR N-PSDB; AAK51462.
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 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 3215-3216; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
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 Best Local Similarity 62.5%; Pred. No. 79;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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 Db ::|||
 97 ILIPVWMF 104

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	38	65.5	246	US-09-709-791-3	Sequence 3, Appli
3	38	65.5	262	US-08-634-475-2	Sequence 2, Appli
4	38	65.5	262	US-09-709-791-2	Sequence 2, Appli
5	34	58.6	591	US-09-352-159-46	Sequence 46, Appli
6	34	58.6	598	US-09-352-159-42	Sequence 42, Appli
7	33	56.9	700	US-08-274-121B-5	Sequence 5, Appli
8	32	55.2	462	US-09-352-159-6	Sequence 6, Appli
9	32	55.2	462	US-09-352-159-8	Sequence 8, Appli
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ALIGNMENTS

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; Patent No. 6143950
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; APPLICANT: Chory et al., Joanne
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; DET2
; TITLE OF INVENTION: DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/634.475
;; FILING DATE: 18-APR-1996
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07251/015001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619/678-5070
;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 246 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-634-475-3

Query Match 65.5%; Score 38; DB 4; Length 246;
Best Local Similarity 45.5%; Pred. No. 8.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
Db 77 RTIYPLRLFR 87

RESULT 2
US-09-709-791-3
; Sequence 3, Application US/09709791
; Patent No. 6352846
; GENERAL INFORMATION:
; APPLICANT: Chory, Joanne
; Li, Jianming
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
; DET2

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/709,791
FILING DATE: 07-NOV-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: SALKINS.010DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/235-8550
TELEFAX: 619/235-0176
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-709-791-3

Query Match 65.5%; Score 38; DB 4; Length 246;
Best Local Similarity 45.5%; Pred. No. 8.3;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
Db 77 RTIYPLRLFR 87

RESULT 3
US-08-634-475-2
; Sequence 2, Application US/08634475
; Patent No. 6143950
; GENERAL INFORMATION:
; APPLICANT: Chory et al., Joanne
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
; DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/634,475
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07251/015001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-634-475-2

Query Match 65.5%; Score 38; DB 4; Length 262;
Best Local Similarity 45.5%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
Db 93 RTIYPLRLFR 103

RESULT 4
US-09-709-791-2
; Sequence 2, Application US/09709791
; Patent No. 6352846
; GENERAL INFORMATION:
; APPLICANT: Chory, Joanne
; Li, Jianming
; TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
; DET2
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th floor
; CITY: Newport Beach

STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/709,791
FILING DATE: 07-NO. 6352846-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: SALKINS.010DVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/235-8550
TELEFAX: 619/235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-709-791-2

Query Match 65.5%; Score 38; DB 4; Length 262;
Best Local Similarity 45.5%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
|:|:|:|:|:
Db 93 RTIYPLRLFR 103

RESULT 5
US-09-352-159-46
; Sequence 46, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rhinocladella atrovirens
US-09-352-159-46

Query Match 58.6%; Score 34; DB 4; Length 591;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:|:|:|:|:
Db 405 TTYLPTLIF 413

RESULT 6

US-09-352-159-42
; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Rhinocladella atrovirens
US-09-352-159-42

Query Match 58.6%; Score 34; DB 4; Length 598;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:|:|:|:|:
Db 406 TTYLPTLIF 414

RESULT 7
US-08-274-121B-5
; Sequence 5, Application US/08274121B
; Patent No. 6133034
; GENERAL INFORMATION:
; APPLICANT: Arne Reider Strom
; APPLICANT: Inga Kaasen
; APPLICANT: Olaf Bay Styrvold
; APPLICANT: John McDougall
; TITLE OF INVENTION: Methods and Compositions
; TITLE OF INVENTION: Related to The Production
; TITLE OF INVENTION: Of Trehalose
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,121B
; FILING DATE: 12-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/893,099
; FILING DATE: 27-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 86(1)
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (916) 753-6113
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-274-121B-5

Query Match 56.9%; Score 33; DB 4; Length 700;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMF 10
: : : : :
Db 672 KAIYPTFF 681

RESULT 8

US-09-352-159-6
; Sequence 6, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-6

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
: : : : :
Db 270 TTLYPTLTF 278

RESULT 9

US-09-352-159-8
; Sequence 8, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8

; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-8

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
: : : : :
Db 270 TTLYPTLTF 278

RESULT 10

US-09-352-168-6
; Sequence 6, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-6

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
: : : : :
Db 270 TTLYPTLTF 278

RESULT 11

US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-8

Query Match 55.2%; Score 32; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 270 TTLXPTLTF 278

RESULT 12
US-09-352-159-11
; Sequence 11, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-11

Query Match 55.2%; Score 32; DB 4; Length 463;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTLXPTLTF 279

RESULT 13
US-09-352-168-11
; Sequence 11, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; OTHER INFORMATION: Extra lysine in the polypeptide sequence of
; OTHER INFORMATION: K:TRAPAO, 463 aa.
US-09-352-168-11

Query Match 55.2%; Score 32; DB 4; Length 463;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 TVVYPTMMF 10
| :|||: |
Db 271 TTLXPTLTF 279

RESULT 14
US-08-959-011-3
; Sequence 3, Application US/08959011
; Patent No. 5932444
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,011
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0412 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 497984
US-08-959-011-3

Query Match 55.2%; Score 32; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVVYPTM 8
| | | | |
Db 244 RTVVPTM 251

RESULT 15
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
US-09-352-159-21

Query Match 55.2%; Score 32; DB 4; Length 487;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:|:|:|
Db 295 TTYLPTLTF 303

RESULT 16

US-09-352-168-21
; Sequence 21, Application US/09352168A
; Patent No. 6211435

; GENERAL INFORMATION:

; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; FILE REFERENCE: 0875

; CURRENT APPLICATION NUMBER: US/09/352,168A

; EARLIER FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: 60/092,936

; EARLIER FILING DATE: 1998-07-25

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 487

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(24)

; OTHER INFORMATION: K:trpAO translational fusion with barley alpha

; OTHER INFORMATION: amylase signal sequence, for expression and

; OTHER INFORMATION: secretion of the mature trpAO in maize.

US-09-352-168-21

Query Match 55.2%; Score 32; DB 4; Length 487;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:|:|:|
Db 295 TTYLPTLTF 303

RESULT 17

US-09-001-826-23

; Sequence 23, Application US/09001826A

; Patent No. 5965727

; GENERAL INFORMATION:

; APPLICANT: SONG, HEE-SOOK
; APPLICANT: BROTHERTON, JEFFREY E.

; APPLICANT: WIDHOLM, JACK M.

; TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE

; FILE REFERENCE: UI001.C1

; CURRENT APPLICATION NUMBER: US/09/001,826A

; CURRENT FILING DATE: 1997-12-31

; EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140

; EARLIER FILING DATE: 1997-07-25; 1996-07-26

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text

; SEQ ID NO 23

; LENGTH: 491

; TYPE: PRT

; ORGANISM: Nicotiana tabacum

US-09-001-826-23

Query Match 55.2%; Score 32; DB 2; Length 491;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
|:|:|:|
Db 422 RTIVFPT 428

RESULT 18

US-09-352-159-17

; Sequence 17, Application US/09352159A

; Patent No. 6211434

; GENERAL INFORMATION:

; APPLICANT: Duwick, Jonathan P.

; APPLICANT: Gilliam, Jacob T.

; APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; FILE REFERENCE: 1134

; CURRENT APPLICATION NUMBER: US/09/352,159A

; CURRENT FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: 60/092,936

; EARLIER FILING DATE: 1998-07-25

; EARLIER APPLICATION NUMBER: 60/135,391

; EARLIER FILING DATE: 1999-05-21

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 554

; TYPE: PRT

; ORGANISM: Exophiala spinifera

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(89)

US-09-352-159-17

Query Match 55.2%; Score 32; DB 4; Length 554;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:|:|:|
Db 362 TTYLPTLTF 370

RESULT 19

US-09-352-168-17

; Sequence 17, Application US/09352168A

; Patent No. 6211435

; GENERAL INFORMATION:

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duwick, Jonathan P.

; APPLICANT: Folkerts, Otto

; APPLICANT: Gilliam, Jacob T.

; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
; OTHER INFORMATION: Yeast alpha mating factor secretion signal.
US-09-352-168-17

Query Match 55.2%; Score 32; DB 4; Length 554;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMFM 10
| :|||: |
Db 362 TTYLPTLTF 370

RESULT 20
US-09-486-382B-2
; Sequence 2, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
; APPLICANT: Hokko Chemical Industry Co., Ltd.
; APPLICANT: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
; TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
; FILE REFERENCE: 10647
; CURRENT APPLICATION NUMBER: US/09/486,382B
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: JP 9-235049
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-486-382B-2

Query Match 55.2%; Score 32; DB 4; Length 577;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
| :|||: |
Db 508 RTIVFPT 514

RESULT 21
US-09-486-382B-13
; Sequence 13, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
; APPLICANT: Hokko Chemical Industry Co., Ltd.
; APPLICANT: MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
; TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
; FILE REFERENCE: 10647
; CURRENT APPLICATION NUMBER: US/09/486,382B
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: JP 9-235049

; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified amino acid sequence of Sequence No. 6388174 2
; Patent No. 6388174
US-09-486-382B-13

Query Match 55.2%; Score 32; DB 4; Length 577;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
| :|||: |
Db 508 RTIVFPT 514

RESULT 22
US-08-604-789B-3
; Sequence 3, Application US/08604789B
; Patent No. 6118047
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; Chomet, P.S.
; Griffor, M.C.
; Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,789B
; FILING DATE: 19-Jan-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 55.2%; Score 32; DB 3; Length 595;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVVYPT 7
||:|:|
Db 526 RTIVFPT 532

RESULT 23

US-09-312-721A-3
; Sequence 3, Application US/09312721A
; Patent No. 6271016

GENERAL INFORMATION:

APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
Kriz, A.L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE

AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
OVERPRODUCTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/312,721A

FILING DATE: 17-May-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/604,789

FILING DATE: 19-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 950.026052

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 373-6903
TELEFAX: (612) 339-3061
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 595 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-312-721A-3

Query Match 55.2%; Score 32; DB 4; Length 595;

Best Local Similarity 71.4%; Pred. NO. 2.7e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVVYPT 7
||:|:|
Db 526 RTIVFPT 532

RESULT 24

US-09-352-159-40

; Sequence 40, Application US/09352159A

; Patent No. 6211434

GENERAL INFORMATION:

APPLICANT: Duwick, Jonathan P.

APPLICANT: Gilliam, Jacob T.

APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (216)...(216)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-352-159-40

Query Match 55.2%; Score 32; DB 4; Length 598;
Best Local Similarity 55.6%; Pred. NO. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|
Db 406 TTYLPTLTF 414

RESULT 25

US-09-352-159-23

; Sequence 23, Application US/09352159A

; Patent No. 6211434

GENERAL INFORMATION:

APPLICANT: Duwick, Jonathan P.

APPLICANT: Gilliam, Jacob T.

APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; FILE REFERENCE: 1134

; CURRENT APPLICATION NUMBER: US/09/352,159A

; CURRENT FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: 60/092,936

; EARLIER FILING DATE: 1998-07-25

; EARLIER APPLICATION NUMBER: 60/135,391

; EARLIER FILING DATE: 1999-05-21

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Exophiala spinifera

; US-09-352-159-23

Query Match 55.2%; Score 32; DB 4; Length 600;

Best Local Similarity 55.6%; Pred. NO. 2.7e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:|:|:|
Db 408 TTYLPTLTF 416

Search completed: July 16, 2003, 14:38:04

Job time : 16 secs

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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:33:19 ; Search time 27.6667 Seconds
(without alignments)
47.218 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFX 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 75 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	34	58.6	322	9	US-10-183-116-16
2	34	58.6	322	9	US-10-079-384-4
3	34	58.6	600	9	US-10-072-307-28
4	34	58.6	600	9	US-10-072-307-30
5	34	58.6	600	9	US-10-072-307-35
6	34	58.6	600	9	US-10-072-307-37
7	34	58.6	600	9	US-10-072-307-40
8	34	58.6	600	9	US-10-072-307-43
9	34	58.6	600	9	US-10-072-307-60
10	34	58.6	600	9	US-10-072-307-64
11	33	58.9	600	9	US-10-072-307-62
12	33	56.9	656	9	US-09-738-626-4577
13	32	55.2	447	9	US-10-169-048-34
14	32	55.2	447	9	US-10-169-048-44
15	32	55.2	462	9	US-09-770-564-6
16	32	55.2	462	9	US-09-770-564-8
17	32	55.2	463	9	US-10-072-307-46
18	32	55.2	463	9	US-10-072-307-47
19	32	55.2	463	9	US-10-072-307-48

20	32	55.2	463	9	US-10-072-307-50
21	32	55.2	463	9	US-09-770-564-11
22	32	55.2	487	9	US-09-770-564-21
23	32	55.2	539	9	US-10-072-307-34
24	32	55.2	554	9	US-09-770-564-17
25	32	55.2	595	10	US-09-733-300-3
26	32	55.2	600	9	US-10-072-307-26
27	32	55.2	600	9	US-10-072-307-27
28	32	55.2	600	9	US-10-072-307-29
29	32	55.2	600	9	US-10-072-307-31
30	32	55.2	600	9	US-10-072-307-32
31	32	55.2	600	9	US-10-072-307-33
32	32	55.2	600	9	US-10-072-307-36
33	32	55.2	600	9	US-10-072-307-38
34	32	55.2	600	9	US-10-072-307-41
35	32	55.2	600	9	US-10-072-307-42
36	32	55.2	600	9	US-10-072-307-44
37	32	55.2	600	9	US-10-072-307-45
38	32	55.2	600	9	US-10-072-307-52
39	32	55.2	600	9	US-10-072-307-54
40	32	55.2	600	9	US-10-072-307-56
41	32	55.2	600	9	US-10-072-307-58
42	32	55.2	600	9	US-10-072-307-66
43	32	55.2	600	9	US-09-770-564-23
44	32	55.2	692	9	US-09-770-564-19
45	32	55.2	829	9	US-09-770-564-33
46	32	55.2	991	9	US-09-770-564-27
47	32	55.2	1000	9	US-09-770-564-25
48	32	55.2	1196	9	US-09-770-564-31
49	32	55.2	1205	9	US-09-770-564-29
50	31	53.4	57	10	US-09-864-761-47860
51	31	53.4	58	9	US-09-764-891-2918
52	31	53.4	157	9	US-09-992-598-103
53	31	53.4	157	9	US-09-989-293A-103
54	31	53.4	157	9	US-09-989-735-103
55	31	53.4	157	9	US-09-990-444-103
56	31	53.4	157	9	US-09-989-730-103
57	31	53.4	157	9	US-09-990-436-103
58	31	53.4	157	9	US-09-991-181-103
59	31	53.4	157	9	US-09-993-687-103
60	31	53.4	157	9	US-09-989-734-103
61	31	53.4	157	9	US-09-997-653-103
62	31	53.4	157	9	US-10-174-590-90
63	31	53.4	157	9	US-10-176-758-90
64	31	53.4	157	9	US-10-175-737-90
65	31	53.4	157	9	US-09-993-667-103
66	31	53.4	157	9	US-10-173-706-90
67	31	53.4	157	9	US-10-173-738-90
68	31	53.4	157	9	US-10-175-752-90
69	31	53.4	157	9	US-10-176-482-90
70	31	53.4	157	9	US-10-176-757-90
71	31	53.4	157	9	US-10-176-913-90
72	31	53.4	157	9	US-10-180-552-90
73	31	53.4	157	9	US-10-180-557-90
74	31	53.4	157	9	US-09-990-438-103
75	31	53.4	157	9	US-09-990-562-103

ALIGNMENTS

RESULT 1
US-10-183-116-16
; Sequence 16, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CAUTE.4C1CP1

; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-16

Query Match 58.6%; Score 34; DB 9; Length 322;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
Db 97 ILYPVMMF 104

RESULT 2

US-10-079-384-4
; Sequence 4, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-4

Query Match 58.6%; Score 34; DB 9; Length 322;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
Db 97 ILYPVMMF 104

RESULT 3

US-10-072-307-28
; Sequence 28, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APL Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324

; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 28
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_F7
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-28

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db 408 TTLPTLIF 416

RESULT 4

US-10-072-307-30
; Sequence 30, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APL Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 30
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G11
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-30

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
Db 408 TTLPTLIF 416

RESULT 5

US-10-072-307-35
; Sequence 35, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APL Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 35
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F15C3
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-35

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||:|
Db 408 TTYLPTLIF 416

RESULT 6

US-10-072-307-37
; Sequence 37, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 37
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F19F2
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-37

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||:|
Db 408 TTYLPTLIF 416

RESULT 7

US-10-072-307-40
; Sequence 40, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73

; SEQ ID NO 40
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F24F2
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-40

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||:|
Db 408 TTYLPTLIF 416

RESULT 8

US-10-072-307-43
; Sequence 43, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 43
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F3B5
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-43

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| :|||:|
Db 408 TTYLPTLIF 416

RESULT 9

US-10-072-307-60
; Sequence 60, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-104020S
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 60

; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocladiaella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 215
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 216
; OTHER INFORMATION: Xaa = Gln, His
US-10-072-307-60

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTWMP 10
| :|||::|
Db 408 TTYLPTLIF 416

RESULT 10
US-10-072-307-64
; Sequence 64, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Davick, Jonathan P.
; TITLE OF INVENTION: AP1 Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072.307
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocladiaella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 13
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 403
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 404
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 419
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 433
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 443
; OTHER INFORMATION: Xaa = Ter, Cys, Trp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 478
; OTHER INFORMATION: Xaa = Leu, Ter, Ser, Trp
; FEATURE:
; NAME/KEY: unsure

; LOCATION: 489
; OTHER INFORMATION: Xaa = Ter, Arg, Gly
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 538
; OTHER INFORMATION: Xaa = Ter, Arg, Gly
US-10-072-307-64

Query Match 58.6%; Score 34; DB 9; Length 600;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTWMP 10
| :|||::|
Db 408 TTYLPTLIF 416

RESULT 11
US-10-072-307-62
; Sequence 62, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Davick, Jonathan P.
; TITLE OF INVENTION: AP1 Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072.307
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Rhinocladiaella atrovirens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 187
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 209
; OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 244
; OTHER INFORMATION: Xaa = Glu, Asp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 262
; OTHER INFORMATION: Xaa = Ter, Cys, Trp
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 295
; OTHER INFORMATION: Xaa = Tyr, Asn, Asp, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 299
; OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 403
; OTHER INFORMATION: Xaa = Val, Leu, Met
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 405
; OTHER INFORMATION: Xaa = Ala, Thr, Pro, Ser
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 409


```
; OTHER INFORMATION: Xaa = Ala, Thr, Ser, Pro
US-10-072-307-62

Query Match          56.9%; Score 33; DB 9; Length 600;
Best Local Similarity 55.8%; Pred. NO. 2.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TVVPTMMF 10
   |::|::|
Db 408 TXLYPTLIF 416

RESULT 12
US-09-738-626-4577
; Sequence 4577, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4577
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4577

Query Match          56.9%; Score 33; DB 9; Length 656;
Best Local Similarity 62.5%; Pred. NO. 3.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
   ::|::|::|
Db 307 IIMPTMMF 314

RESULT 13
US-10-169-048-34
; Sequence 34, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
```

```
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-34

Query Match          55.2%; Score 32; DB 9; Length 447;
Best Local Similarity 45.5%; Pred. NO. 3.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMFK 11
   ::::|::|
Db 190 QTMYPFTFFK 200

RESULT 14
US-10-169-048-44
; Sequence 44, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-44

Query Match          55.2%; Score 32; DB 9; Length 447;
Best Local Similarity 45.5%; Pred. NO. 3.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVYPTMMFK 11
   ::::|::|
Db 190 QTMYPFTFFK 200

RESULT 15
US-09-770-564-6
; Sequence 6, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polycl Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-770-564-6
```

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:||||:|
Db 270 TTLYPTLTF 278

RESULT 16
US-09-770-564-8
; Sequence 8, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-770-564-8

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:||||:|
Db 270 TTLYPTLTF 278

RESULT 17
US-10-072-307-46
; Sequence 46, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 46
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_TrHI
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-46

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:||||:|
Db 271 TTLYPTLTF 279

RESULT 18
US-10-072-307-47
; Sequence 47, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 47
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G6
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-47

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
|:||||:|
Db 271 TTLYPTLTF 279

RESULT 19
US-10-072-307-48
; Sequence 48, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: API Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 48
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_H8
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-48

Query Match 55.2%; Score 32; DB 9; Length 463;

Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :|||: |
Db 271 TTYPTLTF 279

RESULT 20

US-10-072-307-50
; Sequence 50, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 50
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_B6
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-50

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :|||: |
Db 271 TTYPTLTF 279

RESULT 21

US-09-770-564-11
; Sequence 11, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; OTHER INFORMATION: Extra lysine in the polypeptide sequence of
US-09-770-564-11

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :|||: |
Db 271 TTYPTLTF 279

RESULT 22

US-09-770-564-21
; Sequence 21, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:trapAO translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature trapAO in maize.
US-09-770-564-21

Query Match 55.2%; Score 32; DB 9; Length 487;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
| :|||: |
Db 295 TTYPTLTF 303

RESULT 23

US-10-072-307-34
; Sequence 34, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: APl Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 34
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_4F15A11
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-34

Query Match          55.2%; Score 32; DB 9; Length 539;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
Db      347 TTLPTLTF 355

RESULT 24
US-09-770-564-17
; Sequence 17, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
; OTHER INFORMATION: Yeast alpha mating factor secretion signal.
US-09-770-564-17

Query Match          55.2%; Score 32; DB 9; Length 554;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TVVYPTMMF 10
Db      362 TTLPTLTF 370

RESULT 25
US-09-733-300-3
; Sequence 3, Application US/09733300
; Patent No. US20020061570A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, P.C.
; APPLICANT: Chomet, P.S.
; APPLICANT: Griffor, M.C.
; APPLICANT: Kriz, A.L.
; TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
; AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
; OVERPRODUCTION
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
; STREET: P. O. Box 2938
; CITY: Minneapolis
; STATE: MN
```

```
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/733,300
; FILING DATE: 08-Dec-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/312,721
; FILING DATE: 2000-09-11
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 950.026US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6903
; TELEFAX: (612) 339-3061
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-733-300-3

Query Match          55.2%; Score 32; DB 10; Length 595;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVVVPT 7
Db      526 RTIVPT 532

Search completed: July 16, 2003, 14:39:39
Job time : 27.6667 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 20 Seconds
(without alignments)
52.874 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	333	2 S74406	hypothetical prote
2	41	70.7	974	2 T29545	hypothetical prote
3	38	65.5	262	2 C84800	3-oxo-5-alpha-ster
4	38	65.5	394	2 G86657	ABC transporter At
5	37	63.8	395	2 H83424	hypothetical prote
6	35	60.3	180	2 D86267	T6J4.4 protein - A
7	35	60.3	435	2 E72342	pmbA-related prote
8	35	60.3	598	2 AC0890	probable arylsulfa
9	35	60.3	887	2 B96598	hypothetical prote
10	34	58.6	303	2 H84758	hypothetical prote
11	34	58.6	347	2 AD3513	channel protein vi
12	34	58.6	373	2 S17955	long-chain-fatty-a
13	34	58.6	373	2 S15161	long-chain-fatty-a
14	34	58.6	389	2 AD0478	acetylornithine de
15	34	58.6	404	2 B41317	O-antigen ligase c
16	34	58.6	404	2 AE0973	O-antigen ligase [
17	34	58.6	464	2 T50785	nucleoid DNA-bind
18	34	58.6	674	2 D72329	hypothetical prote
19	34	58.6	711	2 A86424	unknown protein, 3
20	33.5	57.8	1724	2 T13942	UNC-13-B protein--
21	33	56.9	120	1 E69798	conserved hypotet
22	33	56.9	136	2 A30710	regulator of nucle
23	33	56.9	136	2 E85560	regulator of nucle
24	33	56.9	136	2 I57917	nucleoside diphosp
25	33	56.9	205	2 S29308	hypothetical prote
26	33	56.9	205	2 F83013	probable transcript
27	33	56.9	221	2 AH0324	probable transcript
28	33	56.9	261	2 T05447	hypothetical prote
29	33	56.9	390	2 AF3425	oxidoreductase (EC

30	33	56.9	394	2 S69870	hypothetical prote
31	33	56.9	531	2 D90453	hypothetical prote
32	33	56.9	551	2 D69282	glutamyl-tRNA synt
33	33	56.9	594	2 S00961	hypothetical prote
34	33	56.9	821	2 B75530	ATP-dependent prot
35	33	56.9	1021	2 T08601	hypothetical prote
36	33	56.9	1235	2 AC1358	ATP-dependent deox
37	33	56.9	1235	2 AC1728	ATP-dependent deox
38	32	55.2	61	1 F2RZKS	photosystem II pro
39	32	55.2	136	2 AC0578	regulator of nucle
40	32	55.2	142	2 G98072	7,8-dihydro-8-oxog
41	32	55.2	143	1 WMBE6H	transcription regu
42	32	55.2	143	2 T43976	transactivator fil
43	32	55.2	169	2 S72166	lipopolysaccharide
44	32	55.2	201	2 T07011	proteinase inhibit
45	32	55.2	203	2 E75413	conserved hypotet
46	32	55.2	214	2 G71318	hypothetical prote
47	32	55.2	214	2 D89985	hypothetical prote
48	32	55.2	214	2 T49174	hypothetical prote
49	32	55.2	283	2 T13879	maturase-like prot
50	32	55.2	283	2 AG1560	hypothetical prote
51	32	55.2	283	2 A11202	hypothetical prote
52	32	55.2	285	2 T09308	immediate-early pr
53	32	55.2	334	2 T44163	hypothetical prote
54	32	55.2	421	2 S26246	glutamate/aspartat
55	32	55.2	458	2 A96938	polyA polymerase I
56	32	55.2	468	2 A55116	vacuolar ATPase (E
57	32	55.2	513	2 T40998	hypothetical prote
58	32	55.2	526	2 T49199	anthranilate synth
59	32	55.2	543	2 T22585	hypothetical prote
60	32	55.2	564	2 S15962	hypothetical prote
61	32	55.2	595	2 J01684	anthranilate synth
62	32	55.2	603	2 T11843	NADH2 dehydrogenas
63	32	55.2	620	2 T21391	hypothetical prote
64	32	55.2	1416	2 D71350	probable DNA-direc
65	32	55.2	1501	2 T29094	ribulose-bisphosph
66	32	55.2	1716	2 T14103	probable DNA-direc
67	32	55.2	3175	1 RRVVEV	genome polyprotein
68	31	53.4	80	2 A60450	hypothetical prote
69	31	53.4	95	2 B83814	Na+/H+ antiporter
70	31	53.4	104	2 T17649	hypothetical prote
71	31	53.4	105	2 T44098	hypothetical prote
72	31	53.4	142	2 G95207	Mutr/nudix family
73	31	53.4	185	2 T29063	hypothetical prote
74	31	53.4	207	2 D65095	hypothetical prote
75	31	53.4	207	2 A98123	hypothetical prote

ALIGNMENTS

RESULT 1

S74406
hypothetical protein sl10456 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74406
O:K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74406
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-333 <KAN>
A:Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAAL0324.1; PID:d101
A>Note: the nucleotide sequence was submitted to the EMBL data Library, June 1996

Query Match 70.7%; Score 41; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 2.8;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|||||:
Db 172 TVVYPTLVF 180

RESULT 2

T29545

hypothetical protein F48C1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29545

R:Gatung, S.; Le, T.T.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid F48C1.

A:Reference number: Z20638

A:Accession: T29545

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-974 <GAT>

A:Cross-references: EMBL:U97015; PIDN:AAB52345.1; GSPDB:GN00019; CESP:F48C1.1

A:Experimental source: strain Bristol N2; clone F48C1

C:Genetics:

A:Gene: CESP:F48C1.1

A:Map position: 1

A:Introns: 15/2; 58/3; 110/3; 150/1; 176/1; 267/2; 296/2; 326/2; 394/3; 441/1; 550/3; 59

Query Match 70.7%; Score 41; DB 2; Length 974;

Best Local Similarity 60.0%; Pred. No. 8.3;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTVYPTMMF 10

|||||
Db 851 QTIYPPMWF 860

RESULT 3

C84800

3-oxo-5-alpha-steroid 4-dehydrogenase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: C84800

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84800

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-262 <STO>

A:Cross-references: GB:AE002093; NID:g4895180; PIDN:AAD32767.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g38050

A:Map position: 2

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match 65.5%; Score 38; DB 2; Length 262;

Best Local Similarity 45.5%; Pred. No. 8.2;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMMFK 11

|||||:
Db 93 RTIYPLRLR 103

RESULT 4

G86657

ABC transporter ATP binding protein ycgB [imported] - Lactococcus lactis subsp. lactis

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: G86657
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; EH
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86657
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <STO>
A:Cross-references: GB:AE005176; PID:g12723123; PIDN:AAK04361.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ycgB

Query Match 65.5%; Score 38; DB 2; Length 394;

Best Local Similarity 66.7%; Pred. No. 12;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10

|||||
Db 47 TLIYPTMRF 55

RESULT 5

H83424

hypothetical protein PAL765 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83424

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83424

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <STO>

A:Cross-references: GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG05154.1; GSPDB:GN

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PAL765

Query Match 63.8%; Score 37; DB 2; Length 395;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTVYPTMMF 10

|||||:
Db 292 RQVVPSPLLF 301

RESULT 6

D86267

T6J4.4 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001

C:Accession: D86267

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86267

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <STO>
 A:Cross-references: GB:AE005172; NID:g9958068; PIDN:AAG09557.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 180;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
 I : ||||| : I
 Db 124 RQLVPTKLF 133

RESULT 7

pmBA-related protein - Thermotoga maritima (strain MSB8)
 E72342
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: E72342
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A:Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: E72342

A>Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-435 <ARN>

A:Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
 A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0727

C:Superfamily: Escherichia coli pmBA protein

Query Match 60.3%; Score 35; DB 2; Length 435;
 Best Local Similarity 54.5%; Pred. No. 53;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 11
 I : I : I : I : I
 Db 135 RVVMPTVMYK 145

RESULT 8

AG0890
 Probable arylsulfate sulfotransferase [imported] - Salmonella enterica subsp. enterica s
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: This species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AG0890

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AG0890

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-598 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD07717.1; PID:g16504269; GSPDB:GN00176

C:Genetics:

A:Gene: STY3370

Query Match 60.3%; Score 35; DB 2; Length 598;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMF 11
 I : I : I : I : I

Db 590 LVHPTOMFK 598

RESULT 9

B96598

hypothetical protein T5A14.3 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: B96598

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 Nature 408, 816-820, 2000

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96598

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-887 <STO>

A:Cross-references: GB:AE005173; NID:g4204259; PIDN:AAD10640.1; GSPDB:GN00141

C:Genetics:

A:Gene: T5A14.3

A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 887;
 Best Local Similarity 70.0%; Pred. No. 1.le+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 11
 I I I I I I I
 Db 696 TVVPTMLK 705

RESULT 10

H84758

hypothetical protein Atg34620 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: H84758

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84758

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303 <STO>

A:Cross-references: GB:AE002093; NID:g3128213; PIDN:AAC26693.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg34620

A:Map position: 2

Query Match 58.6%; Score 34; DB 2; Length 303;
 Best Local Similarity 60.0%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
 I I : I I I
 Db 120 RTELVPVFMF 129

RESULT 11

AD3513

channel protein virB6 homolog [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C;Accession: AD3513
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, P.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AD3513
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-347 <KUR>
 A;Cross-references: GB:AE008918; PIDN:AAL53271.1; PID:g17984152; GSPDB:GN00191
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BMEI10030
 A;Map position: II

Query Match 58.6%; Score 34; DB 2; Length 347;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVPTMMFK 11
 |:| | | |
 Db 257 TVVPMYMYK 266

RESULT 12

S17955
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium leiognathi
 C;Species: Photobacterium leiognathi
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
 C;Accession: S17955
 R;Lee, C.Y.; Szittner, R.B.; Weighen, E.A.
 Eur. J. Biochem. 201, 161-167, 1991
 A;Title: The lux genes of the luminous bacterial symbiont, *Photobacterium leiognathi*, of *Coli*.

A;Reference number: S17836; MUID:92007870; PMID:1915359

A;Accession: S17955
 A;Molecule type: DNA
 A;Residues: 1-373 <LEE>
 A;Cross-references: EMBL:M63594; NID:g150687; PIDN:AAA25620.1; PID:g150692
 C;Genetics:
 A;Gene: luxE
 C;Keywords: acid-thiol ligase

F;364/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 58.6%; Score 34; DB 2; Length 373;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVPTMMFK 11
 |:| | | |
 Db 78 VFPTSMFK 85

RESULT 13

S15161
 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium phd
 A;Alternate names: acyl-protein synthetase
 C;Species: Photobacterium phosphoreum
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C;Accession: S15161
 R;Soly, R.R.; Weighen, E.A.
 J. Mol. Biol. 219, 69-77, 1991

A;Title: Identification of the acyl transfer site of fatty acyl-protein synthetase from *Photobacterium phosphoreum*
 A;Reference number: S15160; MUID:91218179; PMID:2023262
 A;Accession: S15161

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-373 <JMO>

C;Genetics:

A;Gene: luxE

C;Keywords: acid-thiol ligase

F;364/Active site: Cys (covalent substrate-binding) #status predicted

Query Match 58.6%; Score 34; DB 2; Length 373;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVPTMMFK 11
 |:| | | |
 Db 78 VFPTSMFK 85

RESULT 14

AD0478
 acetylornithine deacetylase (EC 3.5.1.16) [imported] - *Yersinia pestis* (strain CO92)
 C;Species: *Yersinia pestis*
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
 C;Accession: AD0478

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-harraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel, N.; Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AD0478

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-389 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC93392.1; PID:g15981838; GSPDB:GN00175

C;Genetics:

A;Gene: argE

C;Superfamily: succinyl-diaminopimelate desuccinylase

C;Keywords: hydrolase

Query Match 58.6%; Score 34; DB 2; Length 389;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVPTMMF 10
 |:| | | |
 Db 238 TIPYPTMNF 246

RESULT 15

B41317

O-antigen ligase complex protein rfaL - *Salmonella typhimurium*

C;Species: *Salmonella typhimurium*

C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999

C;Accession: B41317

R;Machlachian, P.R.; Kadam, S.K.; Sanderson, K.E.

J. Bacteriol. 173, 7151-7163, 1991

A;Title: Cloning, characterization, and DNA sequence of the rfaL region for lipopoly

A;Reference number: A41317; MUID:92041612; PMID:1657881

A;Accession: B41317

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-404 <MAC>

A;Cross-references: GB:IM73826; NID:g154328; PIDN:AAA27206.1; PID:g154330

C;Keywords: transmembrane protein

Query Match 58.6%; Score 34; DB 2; Length 404;
 Best Local Similarity 63.6%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
 |:| | | |
 Db 305 RVVDYPTWTFK 315

RESULT 16

AE0973

O-antigen ligase [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (stra

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AE0973
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A:Reference number: AB0502; PMID:11677608
A:Accession: AE0973
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03281.1; PID:gl6504902; GSPDB:GN00176
C:Genetics:
A:Gene: waaL

Query Match 58.6%; Score 34; DB 2; Length 404;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMFK 11
| | | | |
Db 305 RVDVPTWTFK 315

RESULT 17
T50785
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N:Alternate names: protein T30N20_30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50785
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25240
A:Accession: T50785
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <BEV>
A:Cross-references: EMBL:AL365234
A:Experimental source: cultivar Columbia; BAC clone T30N20
C:Genetics:
A:Map position: 5
A:Introns: 58/1
A:Note: T30N20_30

Query Match 58.6%; Score 34; DB 2; Length 464;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
| | | | |
Db 392 TVTYPTIAF 400

RESULT 18
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
A:Accession: D72329
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: D72329
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-674 <ARN>
A:Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35899.1; PID:g498134
A:Experimental source: strain MSB8

C:Genetics:
A:Gene: TM0817

Query Match 58.6%; Score 34; DB 2; Length 674;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
| | | | |
Db 192 QTFVYVPEMF 201

RESULT 19
A86424
unknown protein, 35070-37205 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A86424
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Mafti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86424
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-711 <STO>
A:Cross-references: GB:AE005172; NID:gl0092467; PIDN:AAG12869.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 58.6%; Score 34; DB 2; Length 711;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
| | | | |
Db 461 RRVYPTLRY 470

RESULT 20
T13942
UNC-13-B protein - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13942
R.Xu, X.Z.; Weis, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C.
J. Biol. Chem. 273, 31297, 1998
A:Title: Retinal targets for calmodulin include proteins implicated in synaptic trans
A:Reference number: Z17709; MUID:99030403; PMID:9813038
A:Accession: T13942
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1724 <XUX>
A:Cross-references: EMBL:Y17922; NID:g3893112; PIDN:CAA76942.1; PID:g3893113
C:Genetics:
A:Cross-references: FlyBase:FBgn0025726
A:Note: UNC-13-B
A:Superfamily: protein kinase C zinc-binding repeat homology
F:602-651/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 57.8%; Score 33.5; DB 2; Length 1724;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 5; Gaps 1;

QY 1 RTVVYPTMMF 11
| | | | |

Db 1437 KTIVLPWTDKTMFK 1452

RESULT 21
E69798
conserved hypothetical protein yeth - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E69798
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toignoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Dauchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69798
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-120 <KUN>
A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12535.1; PID:g2633029
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeth
C:Superfamily: Bacillus probable methylglyoxalase yurt

Query Match 56.9%; Score 33; DB 1; Length 120;
Best Local Similarity 54.8%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 11
I I I I I
Db 53 RLVIYPAKMK 63

RESULT 22
A90710
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A90710
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A90710
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034072.1; PID:g13360107; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: Ecs0649

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
I I I I I
Db 73 RTLVIYPAKM 81

RESULT 23
E85560
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85560
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <STO>
A:Cross-references: GB:AE005174; NID:g12513506; PIDN:AAG54945.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: rnk

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
I I I I I
Db 73 RTLVIYPAKM 81

RESULT 24
I57917
nucleoside diphosphate kinase regulator - Escherichia coli (strain K-12)
N:Alternate names: rnk protein
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 01-Mar-2002
C:Accession: I57917; H64794
R:Schlittman, D.; Shankar, S.; Chakrabarty, A.M.
Mol. Microbiol. 16, 309-320, 1995
A:Title: The Escherichia coli genes sspA and rnk can functionally replace the Pseudom
A:Reference number: I57917; MUID:96015444; PMID:7565093
A:Accession: I57917
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-136 <RES>
A:Cross-references: GB:I37900; NID:g598117; PIDN:AAC36933.1; PID:g598118
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:Cross-references: GB:AE000166; GB:U00096; NID:g1786819; PIDN:AAC73711.1; PID:g17868
A:Experimental source: strain K-12, substrain MGL1655
C:Genetics:
A:Gene: rnk

Query Match 56.9%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
I I I I I
Db 73 RTLVIYPAKM 81

RESULT 25
S29308
hypothetical protein 3 (phac2 3' region) - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999

C:Accession: S29308; S28380
R:Timm, A.; Steinbuechel, A.
Eur. J. Biochem. 209, 15-30, 1992
A:Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus of
A:Reference number: S29303; MUID:93011120; PMID:1396693
A:Accession: S29308
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <TIM>
A:Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47154.1; PID:g45394

Query Match 56.9%; Score 33; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMM 9
|||||
Db 172 RTVYQIMM 180

Search completed: July 16, 2003, 14:34:16
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 10.3333 Seconds
(without alignments)
44.152 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	38	65.5	262	1	DET2_ARATH	Q38944 arabidopsis
2	34	58.6	373	1	LUXE_PHOLE	P29334 photobacter
3	34	58.6	404	1	REFAL_SALTY	P26471 salmonella
4	33	56.9	136	1	RNK_ECOLI	P40679 escherichia
5	33	56.9	193	1	RCF1_DICDI	O96390 dictyosteli
6	33	56.9	551	1	SYE_ARCFU	O29979 archaeoglob
7	33	56.9	594	1	YKP3_KLULA	P05469 kluyveromyc
8	32	55.2	61	1	PSBK_ORYSA	P12162 oryza sativ
9	32	55.2	61	1	PSBK_WHEAT	P58273 triticum ae
10	32	55.2	143	1	B701_HSV6G	P30024 human herpe
11	32	55.2	169	1	COAD_CHRVI	P71154 chromatin
12	32	55.2	200	1	CAKB_COTJA	Q98855 coturnix co
13	32	55.2	201	1	IP23_LYCES	Q43502 lycopersico
14	32	55.2	214	1	Y473_TREPA	O83486 treponema p
15	32	55.2	421	1	GUTT_BACCA	P24944 bacillus ca
16	32	55.2	468	1	VAS1_BOVIN	P40682 bos taurus
17	32	55.2	595	1	TRPE_ARATH	P32068 arabidopsis
18	32	55.2	603	1	NU5M_HYLLA	P03919 hylobates l
19	32	55.2	1416	1	RPOC_TREPA	O83270 treponema p
20	32	55.2	1716	1	RPAI_RAT	O54889 rattus norv
21	32	55.2	3175	1	RPOA_EAV	P19811 equine arte
22	31	53.4	157	1	SMPL_HUMAN	O95807 homo sapien
23	31	53.4	207	1	YOJ1_ECOLI	O46872 escherichia
24	31	53.4	320	1	DNC_HUMAN	Q9hc21 homo sapien
25	31	53.4	362	1	MSPI_YEAST	P28737 saccharomyc
26	31	53.4	421	1	GLTT_BACST	P24943 bacillus st
27	31	53.4	437	1	SECY_BUCAI	P57571 buchnera ap
28	31	53.4	439	1	RHGI_HUMAN	Q07960 homo sapien
29	31	53.4	440	1	AK_CHLPN	O92610 chlamydia p
30	31	53.4	442	1	SECY_SYNY3	P77964 synechocyst
31	31	53.4	507	1	PDI_DATGL	Q9xf61 datisca glo
32	31	53.4	527	1	KITH_HSVSA	P21293 herpesvirus
33	31	53.4	601	1	NU5M_DASNO	O21335 dasypus nov

34	31	53.4	604	1	NU5M_HORSE	P48656 equus cabal
35	31	53.4	606	1	NU5M_BOVIN	P03920 bos taurus
36	31	53.4	606	1	NU5M_CERSI	O03205 ceratotheri
37	31	53.4	606	1	NU5M_BOVAS	P92485 equus asinu
38	31	53.4	606	1	NU5M_SHEEP	O78756 ovis aries
39	31	53.4	640	1	GIDA_ANASU	Q8yr87 anabaena sp
40	31	53.4	657	1	UVRB_CAMJE	Q9ppm7 campylobact
41	31	53.4	714	1	P8PF_BACSU	P38050 bacillus su
42	31	53.4	1067	1	EG52_XENLA	Q91783 xenopus lae
43	31	53.4	3358	1	PGCV_MOUSE	O62059 mus musculu
44	31	53.4	4196	1	DYHC_SCHPO	O13290 schizosacch
45	30.5	52.6	1968	1	RPO_PVMR	P17965 potato viru
46	30	51.7	61	1	PSBK_HORVU	P25872 hordeum vul
47	30	51.7	116	1	LUXE_PHOLU	P19842 photorhabdu
48	30	51.7	122	1	YJ41_YEAST	P47121 saccharomyc
49	30	51.7	149	1	YQBN_BACSU	P45930 bacillus su
50	30	51.7	158	1	IP2X_SOLTU	Q00782 solanum tub
51	30	51.7	193	1	RCF2_DICDI	Q99ps3 dictyosteli
52	30	51.7	221	1	KGY1_BOBBU	O51154 borrelia bu
53	30	51.7	238	1	YG26_HAEIN	P44286 haemophilus
54	30	51.7	265	1	UL07_HSVSA	Q01028 herpesvirus
55	30	51.7	315	1	VC04_YACCV	P17370 vaccinia vi
56	30	51.7	316	1	VC04_VACCC	P21038 vaccinia vi
57	30	51.7	316	1	VC04_VAUV	P34012 variola vir
58	30	51.7	352	1	GLN1_DAUCA	O22504 daucus caro
59	30	51.7	356	1	GLN1_MEDSA	P04078 medicago sa
60	30	51.7	356	1	GLN1_PHAVU	P04770 phaseolus v
61	30	51.7	356	1	GLNA_VIGAC	P32289 vigna aconi
62	30	51.7	358	1	GLNA_LACSA	P23712 lactuca sat
63	30	51.7	376	1	YG3W_YEAST	P32293 saccharomyc
64	30	51.7	378	1	LUXE_VIBHA	P14286 vibrio harv
65	30	51.7	416	1	PXN1_XENLA	P49263 xenopus lae
66	30	51.7	420	1	PUR2_LISIN	Q92ap4 listeria in
67	30	51.7	420	1	PUR2_LISMO	Q8y6c6 listeria mo
68	30	51.7	426	1	STE2_SACKL	P12384 saccharomyc
69	30	51.7	477	1	LXII_HUMAN	Q14108 homo sapien
70	30	51.7	477	1	LXII_RAT	P27615 rattus norv
71	30	51.7	497	1	YJ92_YEAST	P47158 saccharomyc
72	30	51.7	519	1	SNX2_HUMAN	O60749 homo sapien
73	30	51.7	519	1	SNX2_MOUSE	O9cwk8 mus musculu
74	30	51.7	521	1	PELL_SACPS	P79001 saccharomyc
75	30	51.7	536	1	CCM4_DROME	Q9ve00 drosophila

ALIGNMENTS

RESULT 1	DET2_ARATH	STANDARD;	PRT;	262 AA.
ID	DET2_ARATH	Q9SH83;		
AC	Q38944;			
DT	15-JUN-2002	(Rel. 41, Created)		
DT	15-JUN-2002	(Rel. 41, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Probable steroid reductase DET2 (EC 1.3.99.-).			
GN	DET2 OR AR2G38050 OR T8P21.4.			
OS	Arabisopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC	SpERMATOPHYTES; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=9618496; PubMed=8602526;			
RA	Li J., Nagpal P., Vitart V., Morris T.C., Chory J.;			
RT	"A role for brassinosteroids in light-dependent development of			
RT	Arabidopsis."			
RL	Science 272:398-401(1996).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20083487; PubMed=10617197;			

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RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moifaf K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably involved in a reduction step in the
CC biosynthesis of the plant steroid, brassinolide. Defects in DET2
CC leads to defects in light-regulated development.
CC -1- PATHWAY: Brassinolide biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE STEROID 5-ALPHA REDUCTASE FAMILY.
CC
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CC
CC EMBL: U53860; AAC49264.1; -
CC DR EMBL; AC007661; AAD32767.1; -
CC DR EMBL; AY045926; AAK76600.1; -
CC DR EMBL; AY079337; AAL85068.1; -
CC DR InterPro: IPR001104; Strd5A_dhc.
CC DR Pfam: PF02544; Steroid_dh; 1.
CC DR PROSITE; PSS0244; S5A_REDUCTASE; 1.
CC KW Oxidoreductase; Transmembrane.
CC FT TRANSMEM 13 33 POTENTIAL.
CC FT TRANSMEM 51 71 POTENTIAL.
CC FT TRANSMEM 113 133 POTENTIAL.
CC FT TRANSMEM 148 168 POTENTIAL.
CC FT TRANSMEM 205 225 POTENTIAL.
CC FT CONFLICT 198 198 C -> R (IN REF. 1).
CC SQ SEQUENCE 262 AA; 30635 MW; 88291B8A8AF5664 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 262;
Best Local Similarity 45.3%; Pred. No. 1.8;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFK 11
DB 93 RTIYPLRLR 103
II::II :I:

RESULT 2
LUXE_PHOLE
ID LUXE_PHOLE STANDARD; PRT; 373 AA.
AC P29334;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase).
GN LUXE.
OS Photobacterium leiognathi.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC Photobacterium.
OX NCBI_TaxID=658;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25521;
RX MEDLINE=92007870; PubMed=1915359;
RA Lee C.Y., Saittner R.B., Meighen E.A.;
RT "The lux genes of the luminous bacterial symbiont, Photobacterium
RT leiognathi, of the ponyfish. Nucleotide sequence, difference in gene
RT organization, and high expression in mutant Escherichia coli.";
RL Eur. J. Biochem. 201:161-167(1991).
CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein -> AMP + diphosphate +
CC an acyl-protein thioester.
CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC
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CC
CC EMBL: M63594; AAA25620.1; -
CC DR EMBL; S17955; S17955.
CC KW Luminescence; Ligase.
CC SQ SEQUENCE 373 AA; 43099 MW; 1B31848B08BF9921 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 373;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VYPTMFK 11
DB 78 VFPTSMFK 85
II::II III

RESULT 3
RFAL_SALTY
ID RFAL_SALTY STANDARD; PRT; 404 AA.
AC P26471;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE O-antigen ligase.
GN RFAL OR WAAL OR RFBF OR STM3713.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=92041612; PubMed=1657881;
RA MacLachlan P.R., Kadam S.K., Sanderson K.E.;
RT "Cloning, characterization, and DNA sequence of the rfaK region for
RT lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
RL J. Bacteriol. 173:7151-7163(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -1- FUNCTION: ADDS THE O-ANTIGEN ON THE GLUCOSE(II) GROUP OF LPS.
CC -1- PATHWAY: Lipopolysaccharide core biosynthesis.

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: SHOWS ALMOST NO SIMILARITY TO E.COLI RFAL.
CC -----
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CC -----
CC EMBL; M73826; AAA27206.1; -.
CC EMBL; AE008872; AAL22572.1; -.
CC PIR; B41317; B41317.
CC STyGene; SG10340; rfal.
CC Lipopolysaccharide biosynthesis; Ligase; Transmembrane;
KW Complete proteome.
FT TRANSMEM 66 84 POTENTIAL.
FT TRANSMEM 184 203 POTENTIAL.
FT TRANSMEM 227 244 POTENTIAL.
SQ SEQUENCE 404 AA; 46034 MW; 1B84F7B3C757D2AB CRC64;

Query Match 58.6%; Score 34; DB 1; Length 404;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RTVYPTMMFK 11
| | | | |
Db 305 RVDPYPTWTFK 315

RESULT 4
ID RNK_ECOLI STANDARD; PRT; 136 AA.
AC P40679;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of nucleoside diphosphate kinase.
GN RNK OR B0610 OR 20754 OR ECS0649.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96015444; PubMed=7565093;
RA Schlichtman D., Shankar S., Chakrabarty A.M.;
RT "The Escherichia coli genes ssrA and rnk can functionally replace the
RT pseudomonas aeruginosa algininate regulatory gene algR2.";
RL Mol. Microbiol. 16:309-320(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Osfner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

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RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11208551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA
CC ALGINATE REGULATORY GENE ALGR2.
CC -----
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CC -----
CC EMBL; L37900; AAC36933.1; -.
CC EMBL; AE000166; AAC73711.1; -.
CC EMBL; U82598; AAB40810.1; -.
CC EMBL; D90701; BAA35239.1; -.
CC EMBL; D90702; BAA35248.1; -.
CC EMBL; AE005240; AAG54945.1; -.
CC EMBL; AP002552; BAB34072.1; -.
CC EcoGene; EG12637; rnk.
KW Complete proteome.
SQ SEQUENCE 136 AA; 14927 MW; 7043926623BA5E1E CRC64;

Query Match 56.9%; Score 33; DB 1; Length 136;
Best Local Similarity 66.7%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMM 9
| | | | |
Db 73 RLVYPAKM 81

RESULT 5
ID RCFL_DICDI STANDARD; PRT; 193 AA.
AC O96390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAS-related protein racfl.
GN RACFL.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

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NCBI_TaxID=44689;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=99214006; PubMed=10198067;
 Rivero F., Albrecht R., Dislich H., Bracco E., Graciotti L.,
 Bozzaro S., Noegel A.A.;
 "racFl", a novel member of the Rho protein family in Dictyostelium
 discoidium, associates transiently with cell contact areas,
 macropinosomes and phagosomes.";
 Mol. Biol. Cell 10:1205-1219(1999).
 CC -!- FUNCTION: MIGHT ACT IN CONCERT AND/OR SHARE FUNCTIONS WITH OTHER
 CC MEMBERS OF THE RHO FAMILY IN THE REGULATION OF A SUBSET OF
 CC CYTOSKELETAL REARRANGEMENTS THAT ARE REQUIRED FOR THESE PROCESSES.
 CC -!- SUBCELLULAR LOCATION: Membrane-bound.
 CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
 CC
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 CC
 DR EMBL; AF037042; AAD09143.1; -
 DR HSSP; P21181; 1AM4
 DR DictyDb; D072727; racFl.
 DR InterPro; IPR003578; GTPase.Rho.
 DR InterPro; IPR001230; Prenyl-site.
 DR InterPro; IPR001806; Ras.transfmg.
 DR InterPro; IPR005225; Small-GTP.
 DR Pfam; PF00071; ras; 1
 DR PRINTS; PR00449; RASTRNSFRMG.
 DR SMART; SM00174; RHO; 1.
 DR TIGRFAMS; TIGR00231; small-GTP; 1.
 DR GTP-binding; Prenylation; Lipoprotein.
 KW NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 57 61 GTP (BY SIMILARITY).
 FT NP_BIND 115 118 GTP (BY SIMILARITY).
 FT DOMAIN 32 40 EFFECTOR REGION (POTENTIAL).
 FT LIPID 190 190 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 193 AA; 21830 MW; 206E814C823E3B2E CRC64;
 Query Match 56.9%; Score 33; DB 1; Length 193;
 Best Local Similarity 45.5%; Pred. No. 14;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RTVYPTMMFK 11
 Db 173 RSVIYPNKLIK 183
 [1]
 RESULT 6
 SYE_ARCFU STANDARD; PRT; 551 AA.
 AC O29979;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GLURS).
 GN GLTX OR AF0260.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049443; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kervlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Venter J.C.;
 "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus";
 Nature 390:364-370(1997).
 RL -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
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 CC
 DR EMBL; AE001087; AAB90966.1; -
 DR HSSP; P00962; IGTR.
 DR TIGR; AF0260; -
 DR InterPro; IPR004526; GltX.arch.
 DR InterPro; IPR000924; GltX.arch.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR Pfam; PF00749; tRNA-synt_1c; 1.
 DR PRINTS; PR00987; TRNASYNTHGLU.
 DR TIGRFAMS; TIGR00463; gltX.arch; 1.
 DR PROSITE; PS00178; AA-TRNA-LIGASE_I; FALSE_NEG
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 Complete proteome.
 FT SITE 100 "HIGH" REGION.
 SQ SEQUENCE 551 AA; 64402 MW; A985A300C6B68F2E CRC64;
 Query Match 56.9%; Score 33; DB 1; Length 551;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 VVYPTMMFK 11
 Db 270 VVYPTLDFE 278
 [1]
 RESULT 7
 YRP3_KLULA STANDARD; PRT; 594 AA.
 AC P05469;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Hypothetical killer plasmid pGKL-2 protein 3.
 OS Kluyveromyces lactis (Yeast).
 OG Plasmid pGKL-2.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
 RX MEDLINE=88289339; PubMed=3041369;
 RA Tommasino S., Ricci S., Galeotti C.L.;
 "Genome organization of the killer plasmid pGKL2 from Kluyveromyces
 lactis.";
 RL Nucleic Acids Res. 16:5863-5878(1988).
 CC -!- FUNCTION: THE PRESENCE OF THE TWO LINEAR PLASMIDS, TERMED
 CC PGKL1 AND PGKL2, IN STRAINS OF KLUYVEROMYCES LACTIS CONFERS
 CC THE KILLER PHENOTYPE TO THE HOST CELL, BY PROMOTING THE
 CC SECRETION OF A TOXIN ABLE TO INHIBIT THE GROWTH OF SENSITIVE

STRAINS.

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 CC -----

DR EMBL: X07776; CAA30604.1; -;
 DR PIR: S00961; S00961.
 DR InterPro: IPR000977; DNA_ligase.
 DR Pfam: PF01068; DNA_ligase; 1.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 594 AA; 70527 MW; 6AE57D37618BE6B0 CRC64;

Query Match 56.9%; Score 33; DB 1; Length 594;
 Best Local Similarity 36.4%; Pred. No. 45;
 Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTVYPTMMFK 11
 I:|||||
 DB 80 RSTMPSLIFR 90

RESULT 8

PSBK_ORYSA
 ID PSBK_ORYSA STANDARD; PRT; 61 AA.
 AC P12162;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II reaction center protein K precursor (PSII-K).
 GN PSBK.
 OS Oryza sativa (Rice).
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eriactoidae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RX MEDLINE=89364698; PubMed=2770692;
 RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
 RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
 RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiyra M.;
 RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
 RT intermolecular recombination between distinct trna genes accounts for
 RT a major plastid DNA inversion during the evolution of the cereals.";
 RL Mol. Gen. Genet. 217:185-194(1989).
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
 CC OF PHOTOSYSTEM II.
 CC -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.

CC -----
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 CC -----

DR EMBL: X15901; CAA34010.1; -;
 DR PIR: JQ0203; F2RZKS.
 DR InterPro: IPR003687; PSII_PsbK.
 DR Pfam: PF02533; PsbK; 1.
 KW Photosystem II; Chloroplast.
 FT PROPEP 1 24 POTENTIAL.
 FT CHAIN 25 61 PHOTOSYSTEM II REACTION CENTER PROTEIN K.
 SQ SEQUENCE 61 AA; 6982 MW; BBC361067C4158F5 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 61;
 Best Local Similarity 55.6%; Pred. No. 6.9;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 I:|||||
 DB 14 SVIYPTSFF 22

RESULT 9

PSBK_WHEAT
 ID PSBK_WHEAT STANDARD; PRT; 61 AA.
 AC P58273;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Photosystem II reaction center protein K precursor (PSII-K).
 GN PSBK.
 OS Triticum aestivum (Wheat).
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese Spring;
 RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
 RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
 RA Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
 RA Tsunewaki K.;
 RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
 RT complete sequence and contig clones.";
 RL Plant Mol. Biol. Rep. 18:243-253(2000).
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
 CC OF PHOTOSYSTEM II.

CC -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
 CC -----
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 CC -----

DR EMBL: AB042240; BAB47017.1; -;
 DR InterPro: IPR003687; PSII_PsbK.
 DR Pfam: PF02533; PsbK; 1.
 KW Photosystem II; Chloroplast.
 FT PROPEP 1 24 BY SIMILARITY.
 FT CHAIN 25 61 PHOTOSYSTEM II REACTION CENTER PROTEIN K.
 SQ SEQUENCE 61 AA; 7030 MW; 467901067C4158FD CRC64;

Query Match 55.2%; Score 32; DB 1; Length 61;
 Best Local Similarity 55.6%; Pred. No. 6.9;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMMF 10
 I:|||||
 DB 14 SVIYPTSFF 22

RESULT 10

B701_HSV6G
 ID B701_HSV6G STANDARD; PRT; 143 AA.
 AC P30024;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transcriptional regulatory protein B701.
 OS Human herpesvirus (type 6 / strain GS) (HHV6).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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CC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10369;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=92148942; PubMed=1310766;
RA Geng Y., Chandran B., Josephs S.F., Wood C.;
RT "Identification and characterization of a human herpesvirus 6 gene
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter.";
RL J. Virol. 66:1564-1570(1992).
CC -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC HIV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
CC SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
CC DIRECTLY OR INDIRECTLY.
CC -----
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CC -----
DR EMBL; M81789; -; NOT_ANNOTATED_CDS.
DR PUR; A42186; WMBE6H.
KW Transcription regulation; Trans-acting factor; Activator.
SQ SEQUENCE 143 AA; 16385 MW; DQCE4D7C2422AAD8 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 143;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
Db 50 KTLVYKPTMF 59
      :|::|||
      ||

RESULT 11
ID COAD_CHRVI STANDARD; PRT; 169 AA.
AC P71154;
AT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
DE phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
DE pyrophosphorylase).
DE COAD OR KDTB.
GN Chromatium vinosum.
OS Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
OC Allochromatium.
OX NCBI_TaxID=1049;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=D / ATCC 17899 / DSM 180;
RX MEDLINE=96328257; PubMed=8765743;
RA Moulis J.M.;
RT "Molecular cloning and expression of the gene encoding Chromatium
RT vinosum 2[4Fe-4S] ferredoxin.";
RL Biochim. Biophys. Acta 1308:12-14(1996).
CC -!- FUNCTION: REVERSELY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
CC PHOSPHOPANTHETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
CC PYROPHOSPHATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
CC dephospho-CoA.
CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE COAD FAMILY.
CC -----
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CC -----
DR EMBL; U45327; AAC44332.1; -.
DR HSSP; P23875; 1B6T.
DR InterPro; IPR004821; Cyt_tran_rel.
DR InterPro; IPR004820; Cytidylyltransf.
DR InterPro; IPR001980; LPS_biosynth.
DR Pfam; PF01467; Cytidylyltransf; 1.
DR PRINTS; PR01020; LPSBIOSINTSS.
DR TIGRfams; TIGR00125; cyt_tran_rel; 1.
KW Transferase; Nucleotidylyltransferase; Coenzyme A biosynthesis.
SQ SEQUENCE 169 AA; 19559 MW; 5126FD2BF32824AC CRC64;

Query Match 55.2%; Score 32; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVVYP 6
Db 2 RTVVYP 7
      |||||
      |

RESULT 12
ID CAKB_COTJA STANDARD; PRT; 200 AA.
AC Q98855;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative calcium-activated potassium channel beta subunit.
GN CO6.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=97224079; PubMed=9070660;
RA Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT "Suppression in transformed avian fibroblasts of a gene (CO6)
RT encoding a membrane protein related to mammalian potassium channel
RT regulatory subunits.";
RL Oncogene 14:1109-1116(1997).
CC -!- FUNCTION: POTASSIUM CHANNEL PROTEIN WHICH MAY MODULATE THE
CC PROPERTIES OF THE PORE-FORMING ALPHA SUBUNIT (BY SIMILARITY).
CC -!- SUBUNIT: THE CALCIUM-ACTIVATED POTASSIUM CHANNEL IS COMPOSED OF
CC AT LEAST TWO SUBUNITS: A PORE-FORMING ALPHA SUBUNIT AND A
CC REGULATORY BETA SUBUNIT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC -----
DR EMBL; U67865; AAC26967.1; -.
DR InterPro; IPR003930; BK_channel_beta.
DR Pfam; PF03185; CakB; 1.
KW Ionic channel; Transmembrane; Glycoprotein.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 200 AA; 22677 MW; B7A612D8973F711F CRC64;

Query Match 55.2%; Score 32; DB 1; Length 200;

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Best Local Similarity 55.6%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
Db 169 TELWPTLMF 177

RESULT 13
IP23_LYCES
ID IP23_LYCES STANDARD; PRT; 201 AA.
AC Q43502;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteinase inhibitor type II CEVI57 precursor.
GN CEVI57
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rutgers; TISSUE=Leaf;
RA Gadea J., Mayda E., Conejero V., Vera P.;
RT "Characterization of defense-related genes ectopically expressed in
viroid-infected tomato plants.";
RL Mol. Plant Microbe Interact. 9:409-415(1996).
CC -!- INDUCTION: BY VIROID INFECTION.
CC -!- SIMILARITY: BELONGS TO THE POTATO TYPE II PROTEINASE INHIBITOR
FAMILY.
CC
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CC
CC EMBL; X94946; CAA64416.1; -.
DR HSSP; P01080; 45GB.
DR InterPro; IPR003465; Prot_inhib.
DR Pfam; PF02428; Prot_inhib_II; 3.
KW Serine protease inhibitor; Repeat; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 201 PROTEINASE INHIBITOR TYPE II CEVI57.
FT REPEAT 27 83 1.
FT REPEAT 84 143 2.
FT REPEAT 144 199 3.
FT ACT_SITE 32 33 INTERACTION WITH TRYPSIN (PROBABLE).
FT ACT_SITE 147 148 INTERACTION WITH TRYPSIN (PROBABLE).
SQ SEQUENCE 201 AA; 21419 MW; A3FCAB9373D8590 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 201;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVYPT 7
Db 106 KTIYPT 112

RESULT 14
Y473_TREPA
ID Y473_TREPA STANDARD; PRT; 214 AA.
AC O83486;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0473.

TP0473.
GN Treponema pallidum.
OS Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC EMBL; AE001224; AAC65467.1; -.
DR TIGR; TP0473; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 4 23 POTENTIAL.
FT TRANSMEM 35 57 POTENTIAL.
FT TRANSMEM 67 89 POTENTIAL.
FT TRANSMEM 96 118 POTENTIAL.
FT TRANSMEM 128 150 POTENTIAL.
FT TRANSMEM 155 177 POTENTIAL.
FT TRANSMEM 187 209 POTENTIAL.
SQ SEQUENCE 214 AA; 24001 MW; 1497AA7E15DFAE92 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 214;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTVVYPTMM 9
Db 186 RTVVYTSML 194

RESULT 15
GLTT_BACCA
ID GLTT_BACCA STANDARD; PRT; 421 AA.
AC P24944;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier
protein).
GN GLTT.
OS Bacillus caldotenax.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1395;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93062018; PubMed=1359385;
RA Tolner B., Poolman B., Konings W.N.;
RT "Characterization and functional expression in Escherichia coli of
the sodium/proton/glutamate symport proteins of Bacillus
stearothermophilus and Bacillus caldotenax.";
RL Mol. Microbiol. 6:2845-2856(1992).
CC -!- FUNCTION: THIS CARRIER PROTEIN IS PART OF THE NA(+)-DEPENDENT,
BINDING-PROTEIN-INDEPENDENT GLUTAMATE-ASPARTATE TRANSPORT SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.


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CC -!- PATHWAY: Tryptophan biosynthesis; first step.
CC -!- SUBUNIT: Tetramer of two components I and two components II.
CC -!- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC FAMILY.
CC -----
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CC -----
DR EMBL: M92353; AAA32738.1; -.
DR EMBL: AB005237; BAB09667.1; -.
DR PIR: S27751; S27751.
DR HSP: Q06128; IQDL.
DR InterPro: IPR005256; Anth_synth1.
DR InterPro: IPR000350; Chorismate_bind.
DR Pfam: PF00425; chorismate_bind; 1.
DR PRINTS: PR00095; ANTSNTHASE1.
DR ProDom: PD000779; Chorismate_bind; 1.
DR TIGRFAMs: TIGR00564; trpE_most; 1.
DR TrpTophan biosynthesis; Lyase; Chloroplast; Transit peptide;
KW Multigene family.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 595 ANTHRANILATE SYNTHASE COMPONENT I-1.
SQ SEQUENCE 595 AA; 66311 MW; 674175416A2736F0 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 595;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPT 7
||:|:|
DB 536 RTIVFPT 532

RESULT 18
ID NU5M_HYLLA STANDARD; PRT; 603 AA.
AC P03919;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN MTND5 OR ND5 OR NADH5.
OS Hylobates lar (Common gibbon).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Estes;
RA Arnason U., Gullberg A., Xu X.;
RT "A complete mitochondrial DNA molecule of the white-handed gibbon,
RT Hylobates lar, and comparison among individual mitochondrial genes of
RT all hominoid genera."
RL Hereditas 124:185-189(1996).
RN [2]
RP SEQUENCE OF 1-79 FROM N.A.
RX MEDLINE=82242101; PubMed=6284948;
RA Brown W.M., Prager E.M., Wang A., Wilson A.C.;
RT "Mitochondrial DNA sequences of primates: tempo and mode of
RT evolution."
RL J. Mol. Evol. 18:225-239(1982).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----

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CC -----
DR EMBL: X99256; CAA67638.1; -.
DR EMBL: V00659; CAA24025.1; -.
DR PIR: A00449; A00449.
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1; 1.
DR Pfam: PF00662; Oxidored_q1_N; 1.
DR PRINTS: PR01434; NADHDHGNASE5.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
KW SEQUENCE 603 AA; 67360 MW; 3BFF99C6EA7BCE70 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 603;
Best Local Similarity 71.4%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VYPTMMF 10
||:|:|
DB 48 LFPTMMF 54

RESULT 19
ID RPOC_TREPA STANDARD; PRT; 1416 AA.
AC O83270;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR TP0242.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](n).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----

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DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1; 1.
KW RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW Hydrolase; Serine protease; Zinc-finger.
FT CHAIN 1 1727 ORF1A.
FT CHAIN 1728 3175 ORF1B.
FT DOMAIN 1080 1220 TRYPSIN-LIKE SERINE PROTEASE.
FT DOMAIN 1218 1506 HELICASE.
FT DOMAIN 2098 2306 POLYMERASE.
FT ACT_SITE 1103 1103 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1129 1129 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1184 1184 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ZN_FING 2368 2414 BY SIMILARITY.
FT NP_BIND 2528 2535 ATP (BY SIMILARITY).
SQ SEQUENCE 3175 AA; 345275 MW; ED5C8BA0E31DE695 CRC64;

Query Match 55.2%; Score 32; DB 1; Length 3175;
Best Local Similarity 83.3%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 5 YPTMMF 10
DB 1369 YPTMLF 1374
|||||

RESULT 22
SMPL_HUMAN STANDARD; PRT; 157 AA.
AC '095807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small membrane protein 1.
GN SMPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu G.;
RT "A new member of the 18 kDa small membrane protein family in human.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Tissue=Brain;
RC MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansgore W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
[3]
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT VAL-58.
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO C210RF4.
CC
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CC
CC EMBL; AF081282; AAD17754.1; -.
CC EMBL; AL136627; CAB66562.1; -.
DR
```

```
DR EMBL; AF458851; AAL51108.1; -.
DR MIM; 605348; -.
KW Transmembrane; Polymorphism.
FT TRANSMEM 26 46
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 95 115 POTENTIAL.
FT TRANSMEM 126 146 POTENTIAL.
FT VARIANT 58 58 A -> V.
FT VARIANT 141 141 F -> L.
FT SEQUENCE 157 AA; 17400 MW; 8CDF83AA23EBB1FA CRC64;
SQ SEQUENCE 157 AA; 17400 MW; 8CDF83AA23EBB1FA CRC64;

Query Match 53.4%; Score 31; DB 1; Length 157;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VVYPTM 8
DB 44 VVYPTM 49
|||||

RESULT 23
YQJL_ECOLI STANDARD; PRT; 207 AA.
ID YQJL_ECOLI
AC Q46872;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yqjI.
GN YQJL OR B3071.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U28379; AAA89150.1; -.
DR EMBL; AE000389; AAC76106.1; -.
DR EcoGene; EG12954; YQJL.
DR InterPro: IPR005149; PAdr.
DR Pfam; PF03551; PAdr; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 23401 MW; DD3D108D83E087F7 CRC64;

Query Match 53.4%; Score 31; DB 1; Length 207;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
DB 99 VVYPTLDF 106
|||||

RESULT 24
DNC_HUMAN
```


ID AC Q9HC21; DNC_HUMAN STANDARD; PRT; 320 AA.
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling protein 1).
 DE SLC25A19 OR DNC OR MUPL.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RA PubMed=11226231;
 RA Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.;
 RT "The human mitochondrial deoxynucleotide carrier and its role in the toxicity of nucleoside antivirals";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Renard S., Mondesert G., Besnard F.;
 RT "MUP 1, a mitochondrial uncoupling protein";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: responsible for the uptake of deoxynucleotides into the matrix of the mitochondria. Transports all four deoxy NDPs, and, less efficiently, the corresponding dNTPs. Does not transport dNMPs, NMPs, deoxynucleosides, nucleosides, purines, or pyrimidines. Supply deoxynucleotides to the mitochondrial matrix for conversion to triphosphates and incorporation into mitochondrial DNA.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined except for placenta. Highest levels in colon, kidney, lung, testis, spleen, and brain.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Likely to be medically important by providing the means of uptake into mitochondria of nucleoside analogs, leading to the mitochondrial impairment that underlies the toxic side effects of such drugs in the treatment of viral illnesses, including AIDS, and in cancer therapy.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC
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 CC
 DR EMBL; AJ251857; CAC27560.1; -
 DR EMBL; AJ301616; CAC37793.1; -
 DR EMBL; AF182404; AAG16903.1; -
 DR EMBL; BC001075; AAH01075.1; -
 DR EMBL; BC005120; AAH05120.1; -
 DR EMBL; HGNC:14409; SLC25A19.
 DR MIM; 606521; -
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 19 39 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.

FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 173 193 POTENTIAL.
 FT TRANSMEM 293 313 POTENTIAL.
 SQ SEQUENCE 320 AA; 35511 MW; 57CE0F01D538B1BE CRC64;
 Query Match 53.4%; Score 31; DB 1; Length 320;
 Best Local Similarity 45.5%; Pred. No. 61;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RTVVYPTMPFK 11
 Db 231 KLTLYPLDLFK 241
 RESULT 25
 MSPL_YEAST
 ID MSPL_YEAST STANDARD; PRT; 362 AA.
 AC P28737;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE MSPL protein (TAT-binding homolog 4).
 GN MSPL OR YTA4 OR YGR028W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF747-19D;
 RA MEDLINE=94043260; PubMed=8226973;
 RA Nakai M., Endo T., Hase T., Matsubara H.;
 RT "Intramitochondrial protein sorting. Isolation and characterization of the yeast MSPL gene which belongs to a novel family of putative ATPases";
 RL J. Biol. Chem. 268:24262-24269(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA MEDLINE=95274317; PubMed=7754704;
 RA Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnlé S., Schwarzlöse C., Vetter I., Feldmann H.;
 RT "Identification of a set of yeast genes coding for a novel family of putative ATPases with high similarity to constituents of the 26S protease complex";
 RL Yeast 10:1141-1155(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=97435481; PubMed=9290212;
 RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
 RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII";
 RL Yeast 13:1077-1090(1997).
 RN [4]
 RP SEQUENCE OF 280-362 FROM N.A.
 RC STRAIN=SC167;
 RX MEDLINE=92204135; PubMed=1552903;
 RA Lisowsky T.;
 RT "Dual function of a new nuclear gene for oxidative phosphorylation and vegetative growth in yeast";
 RL Mol. Gen. Genet. 232:58-64(1992).
 CC -1- FUNCTION: INVOLVED IN INTRAMITochondrial SORTING OF PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial outer membrane.
 CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
 CC
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DR EMBL; X68055; CAA48191.1; -;
DR EMBL; X81069; CAA56956.1; -;
DR EMBL; X72813; CAA97015.1; -;
DR EMBL; X60722; -; NOT_ANNOTATED_CDS.
DR PIR; S20468; S20468.
DR PIR; S37410; S37410.
DR SGD; S0003260; MSP1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_sub.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW ATP-binding; Mitochondrion; Outer membrane; Transmembrane.
FT DOMAIN 1 12 INTERMEMBRANE (POTENTIAL).
FT TRANSMEM 13 28 POTENTIAL.
FT DOMAIN 29 362 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 133 140 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 40343 MW; 1B3562A32F47F434 CRC64;

Query Match 53.4%; Score 31; DB 1; Length 362;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 TVVYPTMM 9
Db 106 SVIYPLMM 113

Search completed: July 16, 2003, 14:35:16
Job time : 11.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: July 16, 2003, 14:30:45 ; Search time 41.6667 Seconds
(without alignments)
54.396 Million cell updates/sec

Title: US-09-923-716c-4
Perfect score: 58
Sequence: 1 RTVVYPTMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 75 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	333	16 Q55184	Q55184 synecocyst
2	41	70.7	974	5 O01574	O01574 caenorhabdi
3	38	65.5	394	16 Q9CIU3	Q9CIU3 lactococcus
4	37	63.8	390	10 Q8VWX1	Q8VWX1 perilla fru
5	37	63.8	391	10 Q9ZPP7	Q9ZPP7 perilla fru
6	37	63.8	395	16 Q9I2X4	Q9I2X4 pseudomonas
7	36	62.1	512	10 Q9LUC5	Q9LUC5 arabidopsis
8	35	60.3	180	10 Q9FX69	Q9FX69 arabidopsis
9	35	60.3	254	10 Q93ZC5	Q93ZC5 arabidopsis
10	35	60.3	258	10 Q9LS01	Q9LS01 arabidopsis
11	35	60.3	264	16 Q8ZLZ1	Q8ZLZ1 salmonella
12	35	60.3	282	10 Q94JV3	Q94JV3 arabidopsis
13	35	60.3	320	11 Q8VGS2	Q8VGS2 mus musculu
14	35	60.3	435	16 Q9WZ16	Q9WZ16 thermotoga
15	35	60.3	504	12 Q9EME6	Q9EME6 ansacta moo
16	35	60.3	598	16 Q8Z3N6	Q8Z3N6 salmonella

17	35	60.3	705	5 Q8SWA5	Q8swa5 encephalito
18	35	60.3	733	10 Q8S7E2	Q8s7e2 oryza sativ
19	35	60.3	735	10 Q9FJR9	Q9fjr9 arabidopsis
20	35	60.3	887	10 Q9ZVV2	Q9zvv2 arabidopsis
21	35	60.3	1030	3 Q9HFQ9	Q9hfq9 emericella
22	34	58.6	54	12 Q841Z1	Q841z1 influenzavi
23	34	58.6	173	13 Q8U0Z6	Q8uuz6 brachydanio
24	34	58.6	180	16 Q98ID0	Q98id0 rhizobium l
25	34	58.6	212	16 Q8XNC4	Q8xnc4 clostridium
26	34	58.6	217	17 Q9HHU4	Q9hhu4 halobacteri
27	34	58.6	303	10 Q64685	Q64685 arabidopsis
28	34	58.6	316	10 Q9LSV4	Q9lsv4 arabidopsis
29	34	58.6	320	17 Q8U2Z3	Q8u2z3 pyrococcus
30	34	58.6	322	4 Q96LB2	Q96lb2 homo sapien
31	34	58.6	322	4 Q8TDD9	Q8tdt9 homo sapien
32	34	58.6	322	4 Q8TDD8	Q8tdt8 homo sapien
33	34	58.6	347	2 Q9KIS7	Q9kis7 brucella ab
34	34	58.6	347	16 Q8YDZ2	Q8ydz2 brucella me
35	34	58.6	373	2 Q955Z3	P955z3 photobacter
36	34	58.6	373	2 Q52100	Q52100 photobacter
37	34	58.6	389	16 Q8ZA85	Q8za85 versinia pe
38	34	58.6	404	16 Q8Z2F8	Q8z2f8 salmonella
39	34	58.6	464	10 Q9LEW3	Q9lew3 arabidopsis
40	34	58.6	530	17 Q973Z9	Q97z39 sulfolobus
41	34	58.6	674	16 Q9WZS4	Q9wzs4 thermotoga
42	34	58.6	711	10 Q9C8R8	Q9c8r8 arabidopsis
43	33.5	57.8	1304	5 Q96959	Q96959 drosophila
44	33.5	57.8	1508	5 Q8T049	Q8t049 drosophila
45	33.5	57.8	1724	5 Q96960	Q96960 drosophila
46	33.5	57.8	1752	5 Q904K9	Q904k9 drosophila
47	33.5	57.8	1810	5 Q9V483	Q9v483 drosophila
48	33	56.9	120	16 Q31535	Q31535 bacillus su
49	33	56.9	159	8 Q950X8	Q950x8 tetrahymena
50	33	56.9	205	2 Q51516	Q51516 pseudomonas
51	33	56.9	205	16 Q9HUC4	Q9huc4 pseudomonas
52	33	56.9	221	16 Q8ZDB7	Q8zdb7 versinia pe
53	33	56.9	237	10 Q8RX02	Q8rx02 arabidopsis
54	33	56.9	261	10 Q9SUW6	Q9suw6 arabidopsis
55	33	56.9	299	4 Q9NXA8	Q9nxa8 homo sapien
56	33	56.9	310	4 Q9Y6E6	Q9y6e6 homo sapien
57	33	56.9	390	16 Q8YFX4	Q8yfx4 brucella me
58	33	56.9	457	17 Q9HLH0	Q9hlh0 thermoplasma
59	33	56.9	457	17 Q978Q5	Q978q5 thermoplasma
60	33	56.9	474	10 Q43541	Q43541 lilium long
61	33	56.9	531	17 Q97V62	Q97v62 sulfolobus
62	33	56.9	703	12 Q83467	Q83467 porcine ade
63	33	56.9	725	5 Q9VD08	Q9vd08 drosophila
64	33	56.9	821	16 Q9RXG4	Q9rxg4 deinococcus
65	33	56.9	842	17 Q970B4	Q970b4 sulfolobus
66	33	56.9	1021	5 Q15733	Q15733 dictyosteli
67	33	56.9	1063	4 Q8TDZ7	Q8tdz7 homo sapien
68	33	56.9	1235	16 Q929A9	Q929a9 listeria in
69	33	56.9	1235	16 Q8Y511	Q8y511 listeria in
70	33	56.9	1824	5 Q9U0Y5	Q9u0y5 leishmania
71	32	55.2	61	10 Q8S6G8	Q8s6g8 oryza sativ
72	32	55.2	132	8 Q956K0	Q956k0 rhodotorula
73	32	55.2	136	16 Q8XFNO	Q8xfn0 salmonella
74	32	55.2	143	12 Q9WT48	Q9wt48 human herpe
75	32	55.2	143	12 Q9DYD9	Q9dyd9 human herpe

ALIGNMENTS

RESULT 1
Q55184
ID Q55184 PRELIMINARY; PRT; 333 AA.
AC Q55184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein sl10456.
GN SL10456.

```

OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 6803;
RA Tabata S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiyura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D64001; BAA10324.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 333 AA; 37436 MW; 676E7399E4499ED6 CRC64;

Query Match 70.7%; Score 41; DB 16; Length 333;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
Db 172 TVVYPTLVF 180

RESULT 2
O01574 PRELIMINARY; PRT; 974 AA.
AC O01574;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 111.6 kDa protein.
GN F48Cl.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Gattung S., Le T.T.;
RT "The sequence of C. elegans cosmid F48Cl.1.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;

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RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97015; AAB52345.1;
DR InterPro: IPR000602; Glyco_hydro_38.
DR Pfam: PF01074; Glyco_hydro_38; 1.
KW Hypothetical protein.
SQ SEQUENCE 974 AA; 111586 MW; C825EFA33FB2F964 CRC64;

Query Match 70.7%; Score 41; DB 5; Length 974;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTVYPTMMF 10
Db 851 QTIYPTMMF 860

RESULT 3
Q9CIU3 PRELIMINARY; PRT; 394 AA.
AC Q9CIU3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ABC transporter ATP binding protein.
GN YCGB OR LL0263.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006263; AAK04361.1;
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransporterTM.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 394 AA; 43946 MW; 2822CBC28AEA4C36 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 394;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
Db 47 TLIYPTMRF 55

RESULT 4
Q8VWX1 PRELIMINARY; PRT; 390 AA.
AC Q8VWX1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Delta-15 desaturase.
GN FAD3.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.

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OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ORDONG: TISSUE=DEVELOPING SEED;
RA Kim K.-H., Huang S.-K., Huang Y.-S.;
RT "Cloning of Perilla delta-15 desaturase.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213482; AAL36934.1; -
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 2.
SQ SEQUENCE 390 AA; 44857 MW; 6959C941D47A15AB CRC64;

Query Match 63.8%; Score 37; DB 10; Length 390;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TVVYPTMMFK 11
Db 241 TIVGPNMMFK 250

RESULT 5
Q92PP7 PRELIMINARY; PRT; 391 AA.
ID Q92PP7;
AC Q92PP7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Omega-3 fatty acid desaturase.
GN FAD3.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUWON-8;
RX MEDLINE=99205707; PubMed=10189709;
RA Chung C.-H., Kim J.-L., Lee Y.-C., Choi Y.-L.;
RT "Cloning and characterization of a seed-specific omega-3 fatty acid
desaturase cDNA from Perilla frutescens.";
RL Plant Cell Physiol. 40:1114-1118(1999).
DR EMBL; AF047039; AAD15744.1; -
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 2.
SQ SEQUENCE 391 AA; 44931 MW; 6637E81654C17CEC CRC64;

Query Match 63.8%; Score 37; DB 10; Length 391;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TVVYPTMMFK 11
Db 242 TIVGPNMMFK 251

RESULT 6
Q912X4 PRELIMINARY; PRT; 395 AA.
ID Q912X4;
AC Q912X4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA1765.
GN PA1765.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coltray L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RT Nature 406:959-964(2000).
RL EMBL; AE004602; AAG05154.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 395 AA; 44670 MW; FC183A433B2529C8 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 395;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RTVVYPTMMF 10
Db 292 RQVYPSLLF 301

RESULT 7
Q9LUC5 PRELIMINARY; PRT; 512 AA.
ID Q9LUC5;
AC Q9LUC5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Putative cytochrome P450 protein).
GN MIE1.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banho J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Jones T.,
RA Carinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Kim C.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MIE1.20 (GI:9294391).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AB023038; BAB02401.1; -
DR EMBL; AY050827; AAK92762.1; -
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 512 AA; 58442 MW; 19DDEAD9C9BAF0B CRC64;

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Query Match 62.1%; Score 36; DB 10; Length 512;
 Best Local Similarity 63.6%; Pred. No. 90;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 11
 I I I I I I I
 Db 80 RVVPYPIQMFK 90

RESULT 8

Q9FX69 ID Q9FX69 PRELIMINARY; PRT; 180 AA.
 AC Q9FX69;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE T6J4.4 protein.
 GN T6J4.4
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
 RA Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
 RA Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
 RA Lenz C., Liu A., Liu S., Mukharsy N., Pham P., Sakano H., Shinn P.,
 RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AC011810; AAG0957.1; -.
 SQ SEQUENCE 180 AA; 19794 MW; 5DA0943DB333F332 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 180;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
 I I I I I I I
 Db 124 RQLVYPTKLF 133

RESULT 9

Q93ZC5 ID Q93ZC5 PRELIMINARY; PRT; 254 AA.
 AC Q93ZC5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Atgl3280/T6J4_23.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AY057636; AAL15267.1; -.
 SQ SEQUENCE 254 AA; 27809 MW; 4D82FA4889242353 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 254;
 Best Local Similarity 60.0%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
 I I I I I I I
 Db 198 RQLVYPTKLF 207

RESULT 10

Q9LS01 ID Q9LS01 PRELIMINARY; PRT; 258 AA.
 AC Q9LS01;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Genomic DNA, chromosome 3, TAC clone:K13N2.
 GN Arabidopsis thaliana (Mouse-ear cross).
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.,
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 DR ENBL; AB028607; BAA95765.1; -.
 SQ SEQUENCE 258 AA; 28398 MW; 42AF942E0E9AAB87 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 258;
 Best Local Similarity 60.0%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
 I I I I I I I
 Db 202 RQLVYPTKLF 211

RESULT 11

Q8ZLZ1 ID Q8ZLZ1 PRELIMINARY; PRT; 264 AA.
 AC Q8ZLZ1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative arylsulfate sulfotransferase.
 GN STM3192.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Courtney L., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";

RL Nature 413:852-856(2001).
DR EMBL; AE008846; AAL22066.1; .
KW Transferase; Hypothetical protein; Complete proteome.
SQ SEQUENCE 264 AA; 29462 MW; 283F39791813620F CRC64;

Query Match 60.3%; Score 35; DB 16; Length 264;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMFK 11

Db 256 LVHPTQMPK 264

RESULT 12

Q94JV3 ID Q94JV3 PRELIMINARY; PRT; 282 AA.

AC Q94JV3;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE AT5g46920/MQD22.6.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,

RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,

RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,

RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,

RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,

RA Davis R.W., Theologis A., Ecker J.R.;

RT "Arabidopsis cDNA clones."

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF372919; AAK49635.1; .

DR InterPro; IPR000442; Intron_maturase2.

DR Pfam; PF01348; Intron_maturase2; 1.

SQ SEQUENCE 282 AA; 32875 MW; 89B0C6FFA2ABF4B8 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 282;

Best Local Similarity 60.0%; Pred. No. 79;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMMF 10

Db 9 RRVYPTLRY 18

RESULT 13

Q8VGS2 ID Q8VGS2 PRELIMINARY; PRT; 320 AA.

AC Q8VGS2;

DT 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Olfactory receptor MOR187-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;

RT "The olfactory receptor gene superfamily of the mouse."

RL Nat. Neurosci. 0:0-0(2002).

RN [2]

RP SEQUENCE FROM N.A.

RA Adams M.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY073074; AAL60737.1; .
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 320 AA; 36768 MW; 1FF2EBF1413280F1 CRC64;

Query Match 60.3%; Score 35; DB 11; Length 320;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMM 9

Db 82 TVIYPKMM 89

RESULT 14

Q9WZ16 ID Q9WZ16 PRELIMINARY; PRT; 435 AA.

AC Q9WZ16;

DT 01-NOV-1999 (TRENBLrel. 12, Created)

DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE PMBA-related protein.

GN TM0727

OS Thermotoga maritima.

OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

OC NCBI_TaxID=2336;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109;

RA MEDLINE=98287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

RT "Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima."

RL Nature 393:323-329(1999).

DR EMBL; AE001743; AAD35809.1; .

DR TIGR; TM0727; .

DR InterPro; IPR002510; PmbA_TlDD.

DR Pfam; PF01523; PmbA_TlDD; 1.

KW Complete proteome.

SQ SEQUENCE 435 AA; 48306 MW; C8764A342A975819 CRC64;

Query Match 60.3%; Score 35; DB 16; Length 435;

Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVYPTMMFK 11

Db 135 RVVMVPTVMYK 145

RESULT 15

Q9EME6 ID Q9EME6 PRELIMINARY; PRT; 504 AA.

AC Q9EME6;

DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

DE AMV260.

GN AMV260.

OS Amsacta moorei entomopoxvirus (AmEPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;

OC Entomopoxvirus B.

OC NCBI_TaxID=28321;

RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094;
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete Genomic Sequence of the Ansacta moorei Entomopoxvirus:
RT Analysis and Comparison with Other Poxviruses.";
RL Virology 274:120-139(2000).
RN (2)
RP SEQUENCE FROM N.A.
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250284; AAG02966.1; -.
SQ SEQUENCE 504 AA; 61862 MW; ACA9BFFA559FAA50 CRC64;

Query Match 60.3%; Score 35; DB 12; Length 504;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMMFK 11
Db 459 TVIFPSLIFR 468

RESULT 16
Q823N6 PRELIMINARY; PRT; 598 AA.
AC Q823N6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Probable arylsulfate sulfotransferase.
GN STY3370
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627278; CAD07717.1; -.
SQ SEQUENCE 598 AA; 66586 MW; B5434F028A5421F0 CRC64;

Query Match 60.3%; Score 35; DB 16; Length 598;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMFK 11
Db 590 LVHPTQMFK 598

RESULT 17
Q8SWA5 PRELIMINARY; PRT; 705 AA.
AC Q8SWA5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein ECU02_1230.

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GN ECU02_1230.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryoniidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=GB-M1;
MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Raoult G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590442; CAD25152.1; -.
KW Hypothetical protein.
SQ SEQUENCE 705 AA; 79649 MW; 235B834A40258AEF CRC64;

Query Match 60.3%; Score 35; DB 5; Length 705;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVVYPTMM 9
Db 570 TVIYPTLL 577

RESULT 18
Q8S7E2 PRELIMINARY; PRT; 733 AA.
AC Q8S7E2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical 82.3 kDa protein.
GN OSJNEA0057L21.15.
OS Oryza sativa (rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsiirir T., Riggs F., Hsiao J., Zismann V., Blunt S., Pal G.,
RA Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNEA0057L21 genomic sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC087599; AAL79699.1; -.
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82297 MW; 24C8521E18220D9D CRC64;

Query Match 60.3%; Score 35; DB 10; Length 733;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMMF 10
Db 462 RRVVYPTLRY 471

RESULT 19
Q9FJR9 PRELIMINARY; PRT; 735 AA.
ID Q9FJR9

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AC Q9FJR9;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Similarity to maturase-related protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Physically assigned pl and TAC clones.";
RL DNA Res. 5:203-216(1998).
DR EMBL; AB013394; BAB10231.1; -
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF01348; Intron_maturas2; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 735 AA; 85179 MW; 3C4A940CDA6E1590 CRC64;

Query Match 60.3%; Score 35; DB 10; Length 735;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVPTMFK 10
| ||||| :
DB 462 RRVVPTLRY 471

RESULT 20
Q92VV2
ID Q92VV2 PRELIMINARY; PRT; 887 AA.
AC Q92VV2
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE T5A14.3 protein.
GN T5A14.3
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Alkafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Lutos S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005223; AAD10640.1; -
DR HSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 887 AA; 99904 MW; 748B215B02E2E9BC CRC64;

Query Match 60.3%; Score 35; DB 10; Length 887;
Best Local Similarity 70.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMFK 11
| | | | | : |
DB 696 TVVNPFLMK 705
RESULT 21
Q9HFO9
ID Q9HFO9 PRELIMINARY; PRT; 1030 AA.
AC Q9HFO9;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Chitinase.
DE CHIC.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FGSC 4;
RA Specht C.A., Benfield B.B., Garcia J.J.;
RT "Identification of bacteria-like chitinases in fungi.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314225; AAG34171.1; -
DR HSP; P10968; 2CWG.
DR InterPro; IPR001579; Chitinase_18/2.
DR InterPro; IPR001002; Chitin_binding_1.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF00187; Chitin_bind_1; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR ProDom; PD000609; Chitin_binding_1; 1.
DR SMART; SM00270; ChtBD1; 2.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 1030 AA; 112748 MW; 8EE1E64192AF03E5 CRC64;

Query Match 60.3%; Score 35; DB 3; Length 1030;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TVVYPTMFK 10
| | | | | : |
DB 951 TVVPTLTF 959

RESULT 22
Q84121
ID Q84121 PRELIMINARY; PRT; 54 AA.
AC Q84121;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Influenza A/Shearwater/Australia/75 (H5N3), neuraminidase (Seg 6), 5' end (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017869; PubMed=6927853;
RA Blok J., Air G.M.;
RT "Sequence variation at the 3' end of the neuraminidase gene from 39 influenza type A viruses.";
RL Virology 121:211-229(1982).
DR EMBL; K01014; AAA43416.1; -
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 5916 MW; B0BD49BBF05D0153 CRC64;

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Query Match          58.6%; Score 34; DB 12; Length 54;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVVYPTM 8
DB 43 QTVVYPTI 50

RESULT 23
Q8UUZ6          PRELIMINARY; PRT; 173 AA.
AC Q8UUZ6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Alpha A crystallin.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LENS;
RA Runkle S., Hill J., Kantorow M., Horwitz J., Posner M.;
RT "Cloning and characterization of zebrafish (Danio rerio) alpha A-
RL crystallin."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY035778; AAK61363.1;
DR InterPro; IPR001436; Crystallin_alpha.
DR InterPro; IPR003090; Crystallin_N.
DR InterPro; IPR002068; Hsp20.
DR Pfam; PF00525; Crystallin; 1.
DR Pfam; PF00011; HSP20; 1.
DR PRINTS; PR00299; ACRYSTALLIN
DR ProDom; PD001193; Crystallin_N; 1.
DR PROSITE; PS01031; HSP20; 1.
SQ SEQUENCE 173 AA; 19714 MW; 301D743DB91BBC13 CRC64;

Query Match          58.6%; Score 34; DB 13; Length 173;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVVYPTMFM 10
DB 12 RTLGYPTRLF 21

RESULT 24
Q98ID0          PRELIMINARY; PRT; 180 AA.
AC Q98ID0;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein ml12459.
GN MLL2459.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
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RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002999; BAB49586.1;
DR InterPro; IPR005149; PdrR.
DR Pfam; PF03551; PdrR; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 180 AA; 19909 MW; D94F736B2855CF60 CRC64;

Query Match          58.6%; Score 34; DB 16; Length 180;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVYPTMMF 10
DB 49 VVYPTLTF 56

RESULT 25
Q8XNC4          PRELIMINARY; PRT; 212 AA.
AC Q8XNC4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein CPE0414.
GN CPE0414.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003186; BAB80120.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 212 AA; 24363 MW; DB7E1E2AC94BE697 CRC64;

Query Match          58.6%; Score 34; DB 16; Length 212;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVYPTMMFK 11
DB 205 IYPNMIFK 212

Search completed: July 16, 2003, 14:37:07
Job time : 42 secs
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